STIC-Biotech/ChemLib

153748

From:

Hutzell, Paula

Sent:

Wednesday, May 18, 2005 7:07 AM

To: Subject:

Graser, Jennifer; STIC-Biotech/ChemLib

RE: rush search

approved

-----Original Message-----

From:

Graser, Jennifer

Sent:

Tuesday, May 17, 2005 4:48 PM

To: Subject: Hutzell, Paula rush search

Importance: High

Hi Paula,

Could you please authorize this research for an amendment which is due?

Thanks, Jennifer

STIC:

Please search SEQ ID NO: 1 and 2 for Serial No. 10/650,123 in pending and commercial

databases.

Thanks,

Jennifer Graser

REM 3B09 (mailbox 3C18)

Art Unit 1645

272-0858

Interference Search in Exisoffice

STAFF USE ONLY

Online Time:_

Searcher: ______ Searcher Phone: 2-Date Searcher Picked up: _____ Date Completed: _____ Searcher Prep/Rev. Time: ____

NA#:____ AA#:____
Interference:___ SPDI:___
S/L:____ Oligomer:____
Encode/Transl:____

Structure#:_____ Text: Inventor:____ Litigation:___ *******************
Vendors and cost where applicable STN:_____

DIALOG:

QUESTEL/ORBIT:

LEXIS/NEXIS:

SEQUENCE SYSTEM:_____ WWW/Internet:_____ Other(Specify):_____ This Page Blank (Uspto)

AX685933 Sequence AR167417 Sequence AR167420 Sequence U52067 Neisseria m AR167415 Sequence CQ771466 Sequence CQ771466 Sequence CQ771466 Sequence CQ771466 Sequence

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Complete cds
AF175680
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1 (bases 1 to 525)

Moe, G.R., Tan, S. and Granoff, D.M.

Differences in Surface Expression of Neisserial Surface Protein, among Neisseria meningitidis Group B strains

Linfect. Immun. (1999) In press

2 (bases 1 to 525)

Moe, G.R., Tan, S. and Granoff, D.M.

Direct Submission

Submitted (04-AVG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA

Institute, 747 Pifty-Second Street, Oakland, CA 94609, USA
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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Organism="Neisseria meningitidis"
/mol_type="genomic DNA"
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U52066 Neisseria m
AR167414 Sequence
AF175678 Neisseria
AR002420 Neisseria
AX044030 Sequence
U52068 Neisseria m
AR16774 Neisseria
AF175677 Neisseria
AF175676 Neisseria
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Neisserial Surface Protein A strains

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ARLSLARASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKN
VRSGELSVGYRVKF
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1 [1990] In press
2 [bases I to 525]
Noe, G.R., Tan, S. and Granoff, D.M.
                                                                                                                                                                                                                                                                                                                                                                                                           61 GCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTA
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Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0;
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1 (bases 1 to 525)
Moe.G.R., Tan,S. and Granoff,D.M.

Differences in Surface Expression of Neisserial Surface Protein among Neisseria meningitidis Group B strains

2 (bases I to 525)
Moe,G.R., Tan,S. and Granoff,D.M.

Direct Submission
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Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Location/Qualifiers
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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      Length 525;
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100.0%; Score 525; DB 1;
100.0%; Pred. No. 1.5e-96;
iive 0; Mismatches 0;
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/strain="NG6/88"
/db_xref="taxon:487"
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Patent: WO 2004020452-A 8 11-MAR-2004;
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                                                                                                                                                                        /organism="Neisseria meningitidis"
/mol type="unassigned DNA"
/strain="608B"
/db_xref="taxon:487"
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GRSPRISAGYRINDLARPAVDYTRYKNYKAPSTDFKLYSIGASATYDFOTQSPVKPYLG
ARLSINRASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKN
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Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Location/Qualifiers
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/organism="Neisseria meningitidis"
/mol_type="genomic DNA"
/strain="NGP165"
db xref="taxon:487"
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Sequence 1 from Patent W02004019976.
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CQ786532.1 GI:45721576
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| protein id="AAD53286.1"
| db_xref="G1:5825543"
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                                                                                                                                                                     ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
                                                                                                                                            Gaps
GlaxoSmithKline Biologicals S.A. (BE); Utrecht University (NL) Location/Qualifiers
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Plante,M., Cadieux,N., Rioux,C.R., Hamel,J., Brodeur,B.R. and
Martin,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseriaceae, Neisseria.

1 (bases 1 to 830)

Martin,D., Cadieux,N., Hamel,J. and Brodeur,B.R.
Highly conserved Neisseria meningitidis surface protein protection against experimental infection
J. Exp. Med. 185 (7), 1173-1183 (1997)
                                                                                                                                            ;
0
                                                                                                                  Length 525;
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Neisseria meningitidis outer membrane protein gene,
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA
                          1. .525

Organism="Neisseria meningitidis"

/mol type="unassigned DNA"

/db_xref="texcon:487"
                                                                                                               Query Match
100.0%; Score 525; DB 6;
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0;
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U52066.1
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ACCESSION
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KEYWORDS
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/trānslation="wkkalmtlalalpaalaegasgfyvvqadaahakassslgsak
GFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASALYDFDTQSPVKPYLG
ARLSLNRASYDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKN
VRSGELSVGVRVKF"
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                                                                                                                                                                                                                                                                                                                                                                   Submitted (22-MAR-1996) Denis Martin, Department of Microbiology, University Laval, Unite de Vaccinologie, Laboratoire et Service d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705 boul Laurier, Ste-Foy, Quebec GIV 4G2, Canada Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
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3 (bases 1 to 830)
Cadieux,N., Plante,M., Rioux,C.R., Hamel,J., Brodeur,B.R. and
Martin,D.
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                                                                                                           Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer
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100.0%; Pred. No. 1.5e-96;
iive 0; Mismatches 0;
                                                                                                                                                                                          Infect. Immun. 67 (9), 4955-4959 (1999)
99386904
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Neisseriaceae; Neisseria.

S. Moe,G.R., Tan,S. and Granoff,D.M.
Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains
L. Infect. Immun. (1999) In press
E. 2 (bases 1 to 5.2)
S. Moe,G.R., Tan,S. and Granoff,D.M.
Direct Submission
L. Submitted (04-NG-1999) Children's Hospital Oakland Research Institute, 747 Pifty-Second Street, Oakland, CA 94609, USA
Institute, 747 Pifty-Second Street, Oakland, CA 94609, USA
Institute, 747 Pifty-Second Street, Oakland, CA 94609, USA
Institute, 747 Piffy-Second Street, Oakland, CA 94609, USA
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VRSGBLSAGYRVKF.
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                                                                                                                                                                                                                                                                                                                                                                               /organism="Neisseria meningitidis"
/mol_type="genomic DNA"
/strain="CU385"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 99.4%; Score 521.8; DB 1;
Best Local Similarity 99.6%; Pred. No. 6.9e-96;
Matches 523; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
|transi_table=11
|product="surface protein A"
|protein_id="AAD53281.1"
|db_xref="G1:5825531"
                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:487"
1. .525
                                                           Neisseria meningitidis
Neisseria meningitidis
Bacteria; Proteobacteria;
                     GI:5825530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ′gene≃"nspA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="nspA"
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Neisseria meningitidis strain CU385 surface protein A (nspA) gene,
complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      383 TACAGCATCGGCGCGCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTAT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTCGGCGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCCGCAGCGACAGCTTC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGGCGGCGACAGCTTC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACGATTTCAAACTT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACAATCGCCCGTCAAACCGTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 830)
Brodeur,B.R., Martin,D., Hamel,J. and Rioux,C.
Proteinase K resistant surface protein of neisseria meningitidis
Patent: US 6287574-A 1 11-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCCGCTGGCGGAA
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                                                                                                                                                                                   linear
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                                                               GTCCGTTCCGGCGAACTGTCCGTCGCGTGCGCGTCAAATTCTGA
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                                          GTCCGTTCCGGCGAACTGTCCGTCGGCGTCGAATTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pred. No. 1.5e-96;
Matches 525; Conservative 0; Mismatches 0;
                                                                                                                                                                                   DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                            AR167414.1 GI:17903193
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .830
                                                                                                                                                                                                                                                                                                                            Unclassified.
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563
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AF175678
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/product="mafA protein"
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IPFYIFDLADFDGGIADIDNIVGFVSSCRLSKSKKNALTGIAFLRGIDVYDPPISKEK
ALKALEKHPEIYQKFQHFFPFVELPPL"
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YBPGGKYHLFGDPRGSVSDRTGKINVIQDYTHQMGNLLIQQANINGTIGYHTRFSGHG
HEEHAPFDNHAADSASEEKGNVDEGFTVYRLNWEGHEHHPADAYDGPKGGNYPKPTGA
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DRGNSMBFINGVAAGALNPISAGEAVDOMYGENDAAETVBALVNVLPFAKVKNLT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="similar to GP:4838554 percent identity: 79.35; identified by sequence similarity; putative" /codon start=1 /trans1_table=11
                                                                                                                                                                                                                                                                                                         943. .1232
/gene="NMB0651"
/note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="hypothetical protein; identified by Glimmer2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="MafB-related protein; identified by Oxford;
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transl_table=11

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/db_xref="GI:7225879"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             product="MafB-related protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="NMB0652"
1355. .2296
/gene="NMB0652"
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/gene="NMB0654"
3571. .3000
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transl_table=11
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/gene="NMB0653"
                                                                                                                                                                                                                                                           /gene="NMB0651"
843. .1232
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/gene="NMB0653"
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gene="NMB0654"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=1
transl_table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1355. .2296
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Neisseria meningitidis MC58

Neisseria meningitidis MC58

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.

1 (bases 1 to 10057)

2 Tettelin, H., Saunders, N.J., Heidelberg, J., Jeffries, A.C.,
Nelson, K.E., Eisen, J.A., Kethum, K.A., Hood, D.W., Peden, J.F.,
Dodgon, R.G., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, Ba., Mason, T. Ciecko, A., Parksey, D.S., Blair, B.,
Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Complete genome sequence of Neisseria meningitidis serogroup B
strain MC58
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Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
Nelson, K.E., Eisen, J.A., Ketchum, K.A., Hood, D.W., Peden, J.F.,
Dodson, R.J., Nelson, W.C., Gwinn, M.L., DeBoy, R., Peterson, J.D.,
Hickey, E.K., Haft, D.H., Salzberg, S.L., White, O., Fleischmann, R.D.,
Dougherty, B.A., Mason, T., Ciecko, A., Parksey, D.S., Blair, B.,
Cittone, H., Clark, E.B., Cotton, M.D., Utterback, T.R., Khouri, H.,
Qin, H., Vamathevan, J., Gill, J., Scarlato, V., Masignani, V.,
Pizza, M., Grandi, G., Sun, L., Smith, H.O., Fraser, C.M., Moxon, E.R.,
Rappuoli, R. and Venter, J.C.
Direct Submission
L. Submitted (17-MR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
                                                                                                                                                                                             Neisseria meningitidis serogroup B strain MC58 section 62 of 206 of AE002420 AE002098
AE002420 AE00298
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HQDTGRMQLIREGLHHDTGHIGWEAMNKGR"
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       GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA 525
                                              481 GTCCGTTCCGGCGAACTGTCCGCCGGTGTGCGCGTCAAATTCTGA 525
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protein id="AAF41070.1"
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/strain="MC58"
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forganism="Neisseria meningitidis"
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fnote="sequence too long, cut in 8 pieces.~seq 1: 1 to
bases-seq 109: 600001 to 949980 349980 bases-seq 100:
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349980 bases-seq 112: 1500001 to 1849980 bases-seq
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KSRAPTNGQAALDNSVQVKSTSPRRVGVDKANNEIVVLNKTQTFNNGSAEYHGHVRSW
QDLHTDQKNALKKAGLD"
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LSKNKDLDIAGLSLTCFGHLARLHSNIGDYDKVIPLLHSKQDDPELQGRAEDALEDIS
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MPPKPSKPPSTLPPPKPQSWQKR"
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/translation="MKKALATLIALALPAALAEGASGFYVQADAAHAKASSSLGSAK
GFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLG
ARLSLARASVDLGGSBDSFSQTSTGLGVLAGVSXAVTPNVDLDAGYRYNYIGKVNTVKN
VRSGEJASAGVRVKF"
208. . 264
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Brodeur, B.R., Martin, D., Hamel, J. and Rioux, C.
Proteinase K resistant surface protein of neisseria meningitidis
Patent: US 6287574-A 5 11-SEP-2001;
Location/Qualifiers
                                                                                                                                                                                                                    ATGAAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCCGCTGGCAA
                                                                                                                                                                                                                                                                                      TACAGCATCGCCGTCCGCCATTTACGACTTCGACAACCCCAATCGCCCGTCAAACCGTAT
                                                                                                                                                                                                1 ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCCCGGCCGCCGCCGCACTGGCGGAA
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                                                                                                                           Score 518.6; DB 1;
Pred. No. 3e-95;
0; Mismatches 4;
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Best Local Similarity 99.2%;
Matches 521; Conservative
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          90367
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Neisseria meningitidis outer membrane protein gene, complete cds.
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Submitted (22-MR-1996) Denis Martin, Department of Microbiology
Submitted (22-MR-1996) Denis Martin, Department of Microbiology
University Laval, Unite de Vaccinologie, Laboratoire et Service
d'Infectiologie, Centre Hospitalier de l'Universite Laval, 2705
boul Laurier, Ste-Foy, Quebec GIV 4G2, Canada
Location/Qualifiers
                                                                                                                                                                                                  90546 TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCGTTAT
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                                                                            GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
                                                                                                              TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCCATCCACCGATTTCAAACTT
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
1 (bases 1 to 850)
Cadieux,N., Plante,M., Rioux,C.R., Hamel,J., Brodeur,B.R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antibody directed against Neisseria meningitidis NspA outer
membrane protein
Infect. Immun. 67 (9), 4955-4959 (1999)
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/mol_type="genomic DNA"
/strain="Z4063"
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/ccdon_start=1
/transl_table=11
/product="outer membrane protein"
/protein_id="AAB41580.1"
/db_xref="G1:1808967"
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/clone="pNP2205"
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force...NMA0700, possible ribonuclease BN, len: 408 aa; similar to SW.RBN_ECOLI (EMBL:L19201), rbn, Escherichia coli ribonuclease BN (EC 3.1....), fasta acores; E(): 2.3e-28, 34.3% identity in 268 aa overlap Longer than rbn at the C-terminus. Also similar to TR:085449 (EMBL:AF067083) Vitreoscilla sp. hypothetical protein (376 aa), fasta scores; E(): 0, 45.0% identity in 33 aa overlap. Contains a region similar to NMA0677, fasta scores; E(): 44.0% identity in 45 aa overlap. Contains hydrophobic, possible membrane-spanning regions,
                                                                                                                                                                                                                                                                                                                                                                                  /producte "putative periplasmic protein"
/protein_id="CAB83985.1"
/db_xref="C1:7379425"
/db_xref="Uniprot/TrEMBL:09JQQ2"
/translation="MLTKLKILLFPFPFVJAINLLFFFFSSDIESFGNYOFEYVYD
KGWPANYILWKDGNFGNFDKIISGLVLEYYKEDDNIYFSYIDGQGFASDSCYYKPEI
LYGKIILNKNHIININSMEKNNFLSEDKIMKGTRNWLADPKNKCNIQTLD"
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VGSVODAALASGAPOWSGALRTAATLTFWTLLLWGLYRFVPNRFVPARQAFVGALATA
PCLETRASLFTWYMGNRDGYRSIYGAFAAVPFELLWIALLWTLVLGGAVLTSSLSYWO
GEAFRRGFROFLYNTLLLLDAAQKEGKALPVOEFRRHINMGYDELGELLEKLA
RHGYIYSGROGWVLKTGADSIELNELFKLFVYRPLPVERDHVNQAVDAVMMPCLQTLN
MTLAEFDAQAKKQOQS
                                                                                                                                                                                                                                                /note="NWA0698, possible periplasmic protein, len: 152 aa, unknown, contains a probable N-terminal signal sequence and lies within a region of unusually low GC content"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tränslation="MTFLQRLQGLADNKICAFAWFVVRRFDEERVPQAAASMTFTTLL
ALVPVLTVMVAVASIFPVFDRWSDSFVSFVNQTIVPQGADMVFDYINAFREQANRLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
/product="putative_ABC_transporter_protein (pseudogene)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="NMA0699"
/note="NMA0699"
/note="NMA0699, pseudogene, probable ABC transporter protein, len 336 bp; similar to C-termini of many ABC transporters e.g. TR:046973 (EMBL:U47048), mtfB. Escherichia coli microcin transport protein (707 aa), fasta scores; E(): 2.66-19, 33.2% identity in 111 aa overlap. Contains PS00211 ABC transporters family signature. NMA0686 may be the remainder of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="NWA0699"
/note="PS00211 ABC transporters family signature"
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complement(1101. .2327)
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                                                                                                                                                                                            129. .587
/gene="NMA0698"
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/gene="NMA0699"
                                                                                                                                                                     gene="NMA0698"
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120
                                                                                                                      GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 327
                                                                                                                                                                                                                                       328 GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 387
                                                                                                                                                                                                                                                                                                             240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCAGCGACAGCTTC 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGGTTACCCCGGAAT 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            628 GTCGATTTGGATGCCGGCTACCGCTACAACTACAACTACGAAAAGTCGACAAAAGTCAAAAAAC 687
                                                                                                                                                                                               GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180
                                                                                                                                                                                                                                                                                                                                                                 388 TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT 447
                                                                                                                                                                                                                                                                                                                                                                                                                        TACAGCATCGGCGCCTCCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 racadcarcescerececearrascaerrecaececaarcececereaaecerar 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTCGGCGCGCGCGCTTGAGCCTCAACCGCCCTCCGTCGACTTGGGCGGCGGCACGCTTC 360
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Neisseria meningitidis serogroup A strain Z2491 complete genome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Parkhill, J., Achman, M., James, K.D., Bentley, S.D., Churcher, C., Klee, S.R., Morelli, G., Bacham, D., Brown, D., Chillingworth, T., Davis, P.M., Davis, P., Devlin, K., Feltwell, T., Hamlin, N., Holroyd, S., Jagels, K., Leather, S., Moule, S., Mungall, K., Quall, M.A., Rajandream, M.A., Rutherford, K.M., Simmonds, M., Skelton, J., Whitehead, S., Spratt, B.G. and Barrell, B.G. Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Details of N. meningitidis sequencing at the Sanger Centre are available on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/N_meningitidis/).

Location/Qualifiers
1. .311321
                                                                                      GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA
                                                                                                                                                                                                                                                                                                             TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCCATCCACCGATTTCAAACTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing team, Sanger Centre, Wellcome Trust Genome Campus.
Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
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Neisseria meningitidis Z2491
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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1 (bases 1 to 311321)
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AL162754 AL157959
AL162754.2 GI:7379424
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Score 518.6; DB 1
Pred. No. 2.1e-95;
0; Mismatches 4
                                                                                                                       4083. .4505
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4083. .4505
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                                                                                                                                                                                                                                                                                                                                                                  98.8%;
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complete cds.
AF175677
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                                                     misc_feature
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2871...3350
2871...3350
/gene="NNA0702"
/note="NNA0702"
/note="NNA0702"
/note="NNA0702"
/sexB. Rhizobium meliloti putative regulator of succinoglycan biosynthesis (not a transcriptional regulator) (234 aa), fasta accores; E(): 3.1e-15, 32.7$
identity in 205 aa overlap. Also similar to many hbacterial ypothetical proteins e.g. SW:YBAX_HAEIN (EMBL:U32798), HIL191, Haemophilus influenzae hypothetical protein access; E(): 0, 79.2$ identity in 13 aa overlap.
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//hortein id="CABB3989:"
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FLLYAAIYAKGQGHRIIIAGYGTPFSGYPDCRDYFVKSMNYTLNLAMDYDFQLITTP
MYLTKAQTWALADEMGALDYIREQTHTCYNGIVGGCRECPSCILRERGLAEYLESKKA
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/gene="NMA0701"
/note="NMA0701, possible pseudogene, len: 258 bp; shows weak similarity to part of SW:WRBA_ECOLI (EMBL:M99166), wrbA, Escherichia coli Trp repressor binding protein (197 aa), fasta scores; E(): 0.064, 29.3% identity in 82 aa overlap. Also similar to part of TR:085450 (EMBL:AF067083)
                                                                                                                                                                                                                                                                                                                            Vitreoscilla sp. Trp repressor binding protein (fragment) (124 aa), fasta scores; E(): 6.6e-14, 56.6% identity in 83
                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2778. .2787
/note="Core DNA uptake sequence: gccgtctgaa"
                                                                                       2444. 2453
/note="Core DNA uptake sequence: gccgtctgaa"
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/note="Core DNA uptake sequence: gccgtctgaa"
'note="Core DNA uptake sequence: gccgtctgaa"
                                                     gccgtctgaa"
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                                                   'note="Core DNA uptake sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GOA:Q9JVT8"
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                                  .2426)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (2755. .2764)
                                  complement (2417.
                                                                                                                                          2486. .2743
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DADKIHIDGWQVVEWADGYDIAVSETPKTKWPSENAPRLYPANVGGYRAGQIAEAHAF
GLFAAATPAEAKQKALQTLLTDSYVQQHKDNLKDVDNLLALDRIGNFHIRLTPNPHGK
PAEIGFQGYLPI"
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                                                                                                                                                                                                                                                                                                                    /note="NWA0704, len: 140 aa; similar to many hypothetical proteins e.g. SW:YB90 HAEIN (EMBL:102798), H11190, Haemophilus influenze hypothetical protein (141 aa), fasta scores; E(): 5.1e-32, 58.0% identity in 138 aa overlap. Shows very weak similarity to eukaryotic (Expruvoyl-terrahydropterin synthases e.g. SW:PTPS_RAT (EMBL:M77850), pts, Rattus norvegicus 6-pyruvoyl pts, Rattus norvegicus 6-pyruvoyl (144)
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Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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                                                                                                                     /gene="NMA0703"
/note="Core DNA uptake sequence: gccgtctgaa"
/label=DUS
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GRSPRISAGYRINDLAFAYDYTRYKNYKAPSTDFKLYSIGASAIYDFOTQSPVKFYLG
ARLSLURAASUDLGGSDSFSQTSTGLGVLTGVSYAVTFNVDLDAGYRYNYIGKVNTVKN
VRSGELSAGGYRVKF"
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1 (bases 1 to 525)
Moe.G.R., Tan,S. and Granoff,D.M.
Differences in Surface Expression of Neisserial Surface Protein among Neisseria meningitidis Group B strains
Infect. Immun. (1999) In press
2 (bases 1 to 525)
Moe.G.R., Tan,S. and Granoff,D.M.
Direct Submission
Submitted (04-AUG-1999) Children's Hospital Oakland Research
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                                                                                                            Institute, 747 Fifty-Second Street, Oakland, CA 94609, Docation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 517; DB 1; Length 525;
Pred. No. 6.5e-95;
0; Mismatches 5; Indels
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                                                                                                                                                                           meningitidis"
                                                                                                                                                                                                                                                                                           /codon start=1
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/db_xref="G1:5825529"
                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="BZ232"
                                                                                                                                                              1. .525
/organism="Neisseria
                                                                                                                                                                                                                       /db_xref="taxon:487"
1. .525
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99.0%;
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/gene="nspA"
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Matches 520; Conservative
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RESULT

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/trānslation="MKKALATLIALAIPAAALABGASGFYVQADAAHAKASSSLGSAK
GFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGAGAIYDFDTQSPVKPYLG
ARLSINRASVDLGGSDSFSQTSTGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKN
VRSGELSAGVRVKF"
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AF175679 525 bp DNA linear BCT 06-SEP-19
Neisseria meningitidis strain M136 surface protein A (nspA) gene,
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                                                                                                                                                                                                                                                                                                                                                               Losses to 525)
Moe,G.R., Tan,S. and Granoff,D.M.
Direct Submission
Submitted (04-AUG-1999) Children's Hospital Oakland Research
Institute, 747 Fifty-Second Street, Oakland, CA 94609, USA
Location/Qualifiers
                                                                                                                                                                       Neisseria meningitidis
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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/organism="Neisseria meningitidis"
                                                                                                                                                                                                                     Neisseriaceae, Neisseria.

1 (bases 1 to 525)
Moe,Gr., Tan. S. and Granoff,D.M.
among Neisseria meningitidis Group B
Infect. Immun. (1999) In press
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /protein_id="AAD53282.1"
/db_xref="GI:5825534"
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/strain="M136"
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/transT_table=11
/product="surface
                                                                                                AF175679.1 GI:5825533
                                                                                                                                                Neisseria meningitidis
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/gene="nspA"
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520; Conserv
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Search completed: May 19, 2005, 17:22:51 Job time : 7013 secs

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US-10-650-123-1 525 Title: Perfect score:

1 atgaaaaaagcacttgccac......gcgtgcgcgtcaaattctga

525

Scoring table: Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

8780412 Notal number of hits satisfying chosen parameters:

4390206 segs, 2959870667 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* Database

geneseqn1980s:* geneseqn1990s:*

geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* genesegn2002bs:* geneseqn2003as:* geneseqn2002as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:*

geneseqn2003bs:*

Aat39041 Proteinas Abs67381 Neisseria Aat39042 Proteinas Aat39040 Proteinas Abz38961 N. gonorr Ad13425 Neisseria Ad7838960 N. gonorr Ad7838964 Neisseria Abq44816 Oligonucl Abq44817 Oligonucl Adm94375 Wheat ABC Adi39160 Streptomy Adl13427 Neisseria Adl24351 N meningi Aat39039 Proteinas Aca64711 N. mening Adf43315 N. mening Continuation (15 o Continuation (7 of Aaf21608 Neisseria Description ADF43315 AAA81490_14 AAA81490_06 AAF71608 AAT39041 AAT39042 AAT39040 ABZ38961 SUMMARIES ADL13425 ABZ38960 ADJ83984 ABQ44816 ABQ44817 ADM94375 ADI39160 ADL24351 AAT39039 ACA64711 ADL13427 Query Match Length DB 985 1919 86941 110000 37668 51.4 51.4 49.8 Score Result No. υ υ

Abl20354 Drosophil	Adj39303 Plant cDN	Ada71243 Rice gene	Adm40964 Neisseria	Ada69820 Rice gene	Aaz30006 Optimised	Aaz30007 Optimised	Abl16369 Drosophil	7 Continuation (38 o	7 Continuation (38 o	Adm40962 Neisseria	Adl24367 N meningi	Acl14692 DNA clone	Aca38418 Prokaryot	Aca40315 Prokaryot			Abg67797 Listeria	Abg67800 Listeria	Aca40556 Prokaryot	Abg70634 Listeria	O Continuation (21 o	Continuat		
ABL20354	ADJ39303	ADA71243	ADM40964	ADA69820	AAZ30006	AAZ30007	ABL16369	AAI99682 37	AAI99683_37	ADM40962	ADL24367	ACL14692	ACA38418	ACA40315	AAI99682 04	AAI99683_04	ABQ67797	ABQ67800	ACA40556	ABQ70634	AAI99682 20	ABQ69245_19	ADP74211	
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49	48.6	47	46.8	46.4	45.6	45.6	45.6	45.6	45.6	45.2	45	45	45	45	45	45	44.8	44.8	44.8	44.8	44.8	44.8	44.8	
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ALIGNMENTS

Neisserial surface protein A; NspA; refolding; recombinant production; vaccine; subunit vaccine; prevention; diagnosis; meningococcus; invasive bacterial disease; bacteraemia; meningitis; Neisseria gonorrhoeae; gonorrhoeae; mature protein; strain H44/76; antibacterial; gene therapy; gene; ds. 1. .525 /*tag= b /*product= "NspA" 1. .57 /*tag= a |*tag= c /*tag= c /*product= "Mature NspA" Neisseria meningitidis H44/76 NspA gene. Location/Qualifiers Neisseria meningitidis; H44/76. BP. ADL13427 standard; DNA; 525 (first entry) WO2004020452-A2. 03-JUN-2004 sig_peptide mat peptide ADL13427; RESULT 1 ADL13427

28-AUG-2003; 2003WO-EP010085 11-MAR-2004.

(GLAX) GLAXOSMITHKLINE BIOLOGICALS SA (UYUT-) RIJKSUNIV UTRECHT. 30-AUG-2002; 2002GB-00020197.

Poolman J; Goraj K, Feron C, Biemans R, Bos M, Denoel P, Tommassen J, Weynants V;

WPI; 2004-239150/22

P-PSDB; ADL13428,

invention relates to an isolated refolded Neisserial surface protein New refolded NspA protein, useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrheae. Disclosure; Fig 3; 62pp; English

A (Naph) from Neisseria meningitidis or Neisserial gonorthoeae. The invention also relates to the method of refolding an Nsph protein; an alkaline refolding buffer comprising ethanolamine and SB-12 (3-dimethyldodecylammoniopropanesulphonate) for refolding an Nsph protein; a pharmaceutical composition comprising the refolded Nsph protein; a pharmaceutical composition comprising the refolded Nsph protein; a carrier and optionally one or more other Neisserial antigens; a method of preventing or treating a Neisserial infection, an antibody immunospecific for the Nsph protein; and diagnosing a Neisserial infection. Nsph has characteristics which indicate that it is a potential vaccine candidate for the development of subunit vaccines for the treatment of infections caused by Neisseria meningitidis (meningococcus), which causes invasive bacterial diseases such as bacteraemia and meningitis, or Neisseria gonorrhoeae, the causative agent of gonorrhoea. Recombinantly produced proteins are tests and in drug screening. However, recombinantly produced proteins are tests and in drug screening. However, recombinantly produced proteins and yields may be very low due to mis-folding and aggregation of the protein. The method of the invention provides an improved method for refolding the protein.

Neph protein, and it is possible to increase the recovery of active and the form of the invention provides an improved method for refolding the protein. protein form partly purified inclusion bodies in amounts up to 100% without the need for further purification. The refolded Naph Proceen is useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The present sequence represents the NspA gene from Neisseria meningitidis

Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other;

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120 360 GCCGCATCCGCCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 120 GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180 TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT 240 181 TICGCCGICGATIACACGCGCIACAAAACIAIAAAGCCCCAICCACCGAITICAAACII 240 TACAGCATCGCCGCCGTTTTACGACTTCGACACCCAATCGCCCGTCAAACCGTAT 300 241 TACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCAATCGCCCGTCAAACCGTAT 300 CTCGGCGCGCGCGCTTGAGCCTCAACCGCCCTCCGTCGACTTGGGCCGCAGCGACAGCTTC 360 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCGAAT 420 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGCGTAAGCTATGCCCGTTACCCCGAAT 420 GTCGATTTGGATGCCGGCTACCGCTACACTACATCGGCAAAGTCAACACTGTCAAAAAC 480 9 9 1 ATGAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA 1 AIGAAAAAAGGCACTIGCCACACIGATIGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA 61 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA CTCGGCGCGCGCTTGAGCCTCAACCGCGCTCCGTCGACTTGGGCGGCGGCACAGCTTC Gaps .; 0 Score 525; DB 12; Length 525; Pred. No. 4.7e-125; 0; Indels 100.0%; Scc... 100.0%; Pred. No. 4... 0; Mismatches Matches 525; Conservative Local Similarity 241 361 61 121 181 301 361 421 421 Query Match 301

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The present invention relates to a pharmaceutical composition comprising a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608b, where the polypeptide is the Neph protein. The composition is useful for inducing an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection and for treating and/or preventing neisserial infection chosen from N. meningitidis, N. genorrhoeae, N. lactamica and N. polysaccharea. It is useful for treatment or prophylaxis of meningities and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is the Neisseria meningitidis strain GGGGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTTTTA 120 Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N. 1 Angabababacacrificcacacacrigatificccricicciccegecegecacacriged GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 0; Gaps Length 525; Sequence 525 BP; 117 A; 186 C; 119 G; 103 T; 0 U; 0 Other; Indels 481 GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCAATTCTGA 481 GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA ds; gene; NspA; vaccine; antibacterial; meningitis. 100.0%; Score 525; DB 12; 100.0%; Pred. No. 4.7e-125; ive 0; Mismatches 0; meningitidis strain 608B NspA coding sequence. Location/Qualifiers 1. .525 /*tag= a /product= "NspA" Claim 9; Fig 1; 79pp; English. 29-AUG-2003; 2003WO-CA001452. 30-AUG-2002; 2002US-0406980P. ADL24351 standard; DNA; 525 (first entry) (SHIR-) SHIRE BIOCHEM INC. 608B NspA coding sequence. Best Local Similarity 100. Matches 525; Conservative Neisseria meningitidis. WPI; 2004-239123/22. P-PSDB; ADL24352. Martin D, Rioux S; WO2004019976-A2. meningitidis. 03-JUN-2004 11-MAR-2004. ADL24351; Н 61 61 Query Match RESULT ADL243 d ઠે ò 셤 ò g ö

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120 262 180 322 240 382 300 442 360

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A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superantigen; ds; gene; SAq; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy; mammalian cell receptor; cytostatic; tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.
                                                                                                                                                                                                                                                                                                                             GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACAAAAGCCTCAAGCTCTTTA
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Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
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ive 0; Mismatches 0;
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antibody; detection; probe; surface protein; ss.
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Neiserria meningitidis.
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28-NOV-2002

30-MAY-2001; 2001US-00870759.

31-MAY-2000; 2000US-0208128P

(TERM/) TERMAN D S

Terman DS;

WPI; 2003-361759/34. P-PSDB; ABU79079 A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis in T cells and antigen presenting cells.

Disclosure; Page; 167pp; English.

The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces an energy or apoptosis in the T cells and antigen presenting cells (APCS). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (MI) a tumouricidal immunocyte population in vivo in a mammal ceptors for immunosupressive fatly acids, ceramides, divolipids, and producing (MI) a tumouricidal immunocyte population in vivo in a mammal ceptors for immunosupressive fatly acids, ceramides, divolipids, applicable in the creatment of cancer comprising a construct useful in the treatment of cancer comprising a cuperantisen (SAG) nucleoside inserted into a virus, a mammalian T cell useful in the treatment of cancer (Managolipids, apmalicables), comprising a lipid raft conjugated to a superantisen (SAG) nucleoside inserted into a virus in a mammal (By allowing tumour associated lipids to context immunocytes to the host), producing (MI) a tumouricidal immunocyte population ex vivo in a mammal (By allowing a tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population ex vivo in a mammal (By allowing a tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population ex vivo in a mammal (By allowing a tumour associated lipids to context APCs, in which receptors for the tumouricidal population ex vivo in a mammal (By allowing a tumour associated lipids to context APCs, in which adaptor producing a tumour associated lipids to context APCs, in which adaptor producing a tumour associated lipids to context T cells in which adaptor producing the tumouricidal population of T cells, and administering per tumouricidal population of T cells which administering the tumouricidal activated T cells ex vivo, in a mammal (By administering the tumouricidal population and proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a fusion constructs with anti-tumour proteins or motifs. The present sequence encodes an anti-tumour protein which is co-administered with or incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent incorporate to the printed specification, but was obtained in electronic format from the US patnet office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551" superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as tumour associated antigen to contact immunocytes in which adaptor

x os	Sequence 830 BP; 210 A; 261 C; 175 G; 184 T; 0 U; 0 Other;
O m ž	Query Match 100.0%; Score 525; DB 8; Length 830; Best Local Similarity 100.0%; Pred. No. 5.3e-125; Matches 525; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
& 8 	1 ATGAAAAAAGCACTTGCCACACTGATTGCCTTCGCTCTCCCGGCCGCGCGCACTGGCGGAA 60
상 원	61 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACGCA
& 8 8	121 GGTTCTGCCAAAGGCTTCAGCCCGCACATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180
& 8 -	181 TTGGCGGTGGATTACACGGGCTACAAAACTATAAAGCCCCATCCACGATTTCAAACTT 240
\$ A	241 TACAGCATCGGCGTCCGCCATTTACGACTTCGACACCCCATCGCCGTCAAACCGTAT 300
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\$ A	361 AGCCAAACCTCCATCGGCCTCGGCGTATTCACGGGCGTAAGCTATGCCGTTACCCCGAAT 420
کہ م	421 GTGGATTTGGATGCCGGCTACCGCTACACTACATCGGCAAAGTCAACACTGTCAAAAAC 480
o d	481 GTCCGTTCCGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA 525
RESI ADF ID	RESULT 5 ADF43315 ID ADF43315 standard; DNA; 830 BP.
ZX A	ADF43315; 12-FEB-2004 (first entry)
XEX	N. meningitidis lipopolysaccharide DNA seq id 35.
\$ & & & \$	receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; lipopolysaccharide; LPS; ds.
* 8 ¥	Neisseria meningitidis.
X A X	US2003157113-A1.
XX F	21-Aug-2003. 28-DEC-2000, 2000US-00751708.
X & \$	28-DEC-1999; 99US-0173371P.
48	(TERM/) TERMAN D S.
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                                                                                                                                                                  The invention describes a receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This sequence encodes Neisseria meningitidis lipopolysaccharide (LPS) to which tumour cells develop
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                                             New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
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                                                                                                                                  Disclosure; SEQ ID NO 35; 151pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis; Neisseria gonorrheae; immunogenic; vaccine;
diagnosis; antigen; detection; infection; gene therapy; antibacterial;
                                                                                                                                   00725 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA
                                                                                                                                                                                                             GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
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Scarselli M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis B nucleotide sequence SEQ ID NO:109.
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ti C, Mora M, Ratti G,
CM, Grandi G;
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AAF21608 standard; DNA; 349980
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08-OCT-1999; 99WO-US023573.
28-FEB-2000; 2000GB-00004695.
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Masignani V, Galeotti C
Rappuoli R, Frazer CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Neisseria meningitidis
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The present invention describes the full length genome of Neisseria meningitidis B (NMB). The sequences in AAF21544 and AAF21607 to AAF21613 cepresent fragments of the NMB genomic sequence, as the sequence was too long to go in a record on its own it was split into 8 sequences which coverlap each other at the beginning and end of each sequence by 49980 bp (1.e. the last 49980 bp of AAF21507 are repeated at the beginning of AAF21607, the last 49980 bp of AAF21607 are repeated at the beginning of AAF21609, and so on). AAF21545 to AAF21589 to AAF21606 represent portains priven in AABS8550 to AABS8593, and AAF21589 to AAF2160 frepresent portains primers which are used in the exemplification of the present invention. The NMB genome and fragments from it have antibacterial activity, and can be used in vaccines and gene therapy. Neisserial nucleic acids, proteins and/or antibodies which binds to the proteins can be used in compositions for treating or preventing infection due to Neisserial bacteria or as diagnostic reagent for detecting the presence of Neisserial bacteria or of antibodies raised to Neisserial bacteria computer storage medium or computer databases can be used in a search to identify open reading frames (ORFs) or coding sequences within the NMB genome. The DNA sequences provide further opportunities to find antigenic or immunogenic proteins which are more effective in vaccines than the computer membrane proteins currently used
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Neisseria meningitidis B full length genome sequence and open reading frames are used to detect, treat and prevent Neisserial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90666 GGITCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
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                                                                   Claim 7; Appendix A; 692pp; English
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Matches 523; Conservative
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RESULT 9 AAT39041 ID AAT39041 standard; DNA; 850 360 567 420 627 480 687

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The present invention relates to a new gram-negative bacterial bleb presenting on its surface the PorB outer membrane protein from Chlamydia trachomatis, or a protective antigen from C. pneumoniae. The invention is useful for preventing C. trachomatis or C. pneumoniae infection in a host. The present nucleic acid sequence represents a Neisseria gonorrhoeae gene as described in the invention
388 TTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTT 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel gram-negative bacterial bleb presenting on its surface PorB outen membrane protein from Chlamydia trachomatis or protective antigen from Chlamydia pneumoniae, useful for preventing Chlamydia infection.
                                                            TACAGCATCGGCGTCCGCCATTTACGACTTCGACACCCCAATCGCCCGTCAAACCGTAT
                                                                                                                         CTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCGGCAGCGACAGCTTC
                                                                                                                                              CTCGGCGCGCGCGTTGAGCCTCAACCGCGCCTCCGTCGACTTTGGGCGCACAGCGACAGCTTC
                                                                                                                                                                                                       361 AGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGGTTACCCCGAAT
                                                                                                                                                                                                                                         AGCCAAACCTCCACCGCCTCGGCGTATTGGCGGGCGTAAGCTATGCCGTTACCCCGAAT
                                                                                                                                                                                                                                                                                         GTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gram-negative bacterial bleb; PorB; outer membrane protein;
Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
protective antigen; antibacterial; vaccine; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 95.7%; Score 502.6; DB 6; Best Local Similarity 97.3%; Pred. No. 2.9e-119; Matches 511; Conservative 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3erthet FJ, Lobet Y, Poolman J, Verlant VGCL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neisseria gonorrhoeae outer membrane gene #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 54; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                           reistant; Neisseria meningitidis; Neisseria gonorrhoeae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
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                                                                                                                    Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 850 BP; 208 A; 273 C; 185 G; 184 T; 0 U; 0 Other;
                                                                                                                                                                                   antibody; detection; probe; surface protein; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rioux C;
                                                                                                                                                                                                                      Neisseria meningitidis; strain 24063
                                                                                                                                                                                                                                                                   Location/Qualifiers
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95US-0001983P.
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Matches 521; Conservative
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                                                            (revised)
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P-PSDB; AAW04893.
                                                                                                                                                           Proteinase K
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A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or thair fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
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                                                            Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
                                                                                                                                                                                                                                                                                                                                                                    Score 502.6; DB 2; Length 810;
Pred. No. 3e-119;
0; Mismatches 14; Indels 0
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                                                                                                                                   Claim 12; Fig 10; 117pp; English.
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milarity 97.3%;
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(first entry)
              WPI; 1996-443187/44.
P-PSDB; AAW04894.
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Matches 511; Conserv
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22-DEC-1996
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antibody; detection; probe; surface protein; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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95US-0001983P.
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/*tag= a
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241. .297
/*tag= b
298. .762
/*tag= c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-1995;
04-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IAFB-) IAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2003
22-DEC-1996
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Gaps

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300 120 180 420 240 480 300 540 360 900 420 9 535

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595

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The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
                                                                                     AATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAA
                                                                                                                                                               AATGTCGATTTGGATGCCGGCTACCGTACAACTACATCGGCAAAGTCAACACTGTCAAA
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                                                         TTCAGCCAAACCTCCATCGGCCTCCGCCTATTGACGGCGTAAGCTATGCCGTTACCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3,
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                                                                                                                                                                                                     525
                                                                                                                                                                                                                                        AATGICCGITCCGGCGAACIGICCGCCGGCGIACGCGICAAATICIGA 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibacterial; infection; vaccine; gene therapy; gene; ds.
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                                                                                                                                                                                                       AACGTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 480.2; DB 10; Length
Pred. No. 1.5e-113;
0; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               N. gonorrhoeae nucleotide sequence SEQ ID 2511
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                                                                                                                                                                                                                                                                                                                                   BP.
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Best Local Similarity 96.0%;
Matches 504; Conservative
                                                                                                                                                                                                                                                                                                                                     525
                                                                                                                                                                                                                                                                                                                                   ABZ38961 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fontana MR, Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-058415/05.
                                                                                                                                                                                                                                                                                                                                                                                                           (first
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                                                                                                                                                                                                                                                                                                                                                                       ABZ38961;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    298 TATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCGCGACAGC 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCGCCGTCGATTACACGCGCTACAAAACTATAAAACAGTCCCATCCACCGATTTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCGCCGTCGATTACACGCGCTACAAAAACTATA---AAGCCCCATCCACCGATTTCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTTACAGCATCGGCGCTCCGCCATTACGACTTCGACACCCCAATCCCCCGTCAAACCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATGAAAAAAGCACTTGCCACCACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
                   » K reistant, Neisseria meningitidis; Neisseria gonorrhoeae;
detection; probe; surface protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                э;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 710 BP; 174 A; 232 C; 148 G; 156 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 491.2; DB 2;
Pred. No. 2.5e-116,
0; Mismatches 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rioux
                                                                            Neisseria meningitidis; strain MCH88
                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 12; Fig 8; 117pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Martin D, Hamel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.6%;
                                                                                                                                                                                                                                                                                                                                                                       95US-00406362
95US-0001983P
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                                                                                                                                 116. .643
/*tag= a
116. .172
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173. .640
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Matches 512; Conservative
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04-AUG-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brodeur BR,
                                                                                                                                                                                                                                                                                                 26-SEP-1996
                                                                                                                                                                   sig_peptide
                                                                                                                                                                                                         mat peptide
                        Proteinase
                                      antibody;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 AATGTCGATCTGGATGCCGGCTACCGCTACAACTACGTCGGCAAAGTCAACAAGAAGTCAAA 480
  GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        surface protein A; NspA; refolding; recombinant production;
                               GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC
                                                                                                                                                TTCGCCGTCGATTACACGCGCTACAAAACTATAAACAAGCCCCATCCACCGGTTTTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                         TTCAGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGGTTACCCCG
                                                                                                           TTCGCCGTCGATTACACGCGCTACAAAACTATA----AAGCCCCATCCACCGATTTCAAA
                                                                                                                                                                                                                    CTTTACAGCATCGGCGTCCGCCATTTACGACTTCGACCCCAATCGCCCGTCAAACCG
                                                                                                                                                                                                                                                                          CTTTACAGCATCGGCGCGTCCGTCATTTACGACTTCGACACCCAATCGCCCGTCAAACCG
                                                                                                                                                                                                                                                                                                                                TATCTCGGCGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCGGCACAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccine; subunit vaccine; prevention; diagnosis; meningococcus; invasive bacterial disease; bacteraemia; meningitis; Neisseria gonorrhoea; gonorrhoea; mature protein; strain H44/76; antibacterial; gene therapy; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Poolman J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AACGTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTC 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria meningitidis H44/76 mature NspA-encoding DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Υ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /partial
/product= "Mature NspA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feron C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'product= "Mature NspA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLAX ) GLAXOSMITHKLINE BIOLOGICALS SA (UYUT-) RIJKSUNIV UTRECHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Neisseria meningitidis; H44/76
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The Invention relates to an insolated relocated with serial suitable process. The invention relates to the method of refolding an NspA protein; an alkaline refolding buffer comprising ethanolamine and SB-12 (3-dimethyldodecylammoniopropaneaulphonate) for refolding an NspA protein; and dimethyldodecylammoniopropaneaulphonate) for refolding an NspA protein, a carrier and optionally one or more other Neisserial antigens; a method of preventing or treating a Neisserial infection. NspA has conferential composition comprising a Neisserial infection. NspA has conferential or treating a Neisserial infection. NspA has consed by Neisseria meningitidis (meningococcus), which causes invasive for the development of subunit vaccines for the treatment of infections cansed by Neisserial meningitidis (meningococcus), which causes invasive consed by Neisserial diseases such as bacteraemia and meningitis, or Neisserial councinged by Neisserial diseases such as bacteraemia and meningitics or Neisserial diseases such as bacteraemia and meningitics or Neisserial could therefore be used to produce vaccine compositions and it could also be used in the development of new antimicrobial agents, diagnostic tests and in drug screening. However, recombinantly produced proteins are frequently unable to adopt their biologically active conformations, and conformation provides an improved method for refolding the NspA protein, and it is possible to increase the recovery of active NspA protein, and it is possible to increase the recovery of active without the need for further purification. The refolded NspA protein is useful for preparing a composition for diagnosing, treating or preventing treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorance warrance was a second method for refolding the warrance warrance warrance warrance 
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                                                                                                                                                                                The invention relates to an isolated refolded Neisserial surface protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      present sequence represents DNA encoding the mature NspA protein from Neisseria meningitidis H44/76 which was amplified and cloned in an example of the invention.
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                        New refolded NspA protein, useful for preparing a composition for
diagnosing, treating or preventing infection caused by Neisseria
meningitidis or Neisseria gonorrheae.
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Pred. No. 1.4e-109;
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                                                                                                                           Example 1; Fig 2; 62pp; English
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99.6%;
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AACGICCGITICCGGCGAACTGICCGCCGGTGTGCGCGTCAATTCTGA

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New protein from Neisseria gonorrheae, useful for the manufacture of medicament for treating or preventing N. gonorrheae infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 368; DB 10; Length 486; Pred. No. 1e-84; 0; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 486 BP; 101 A; 107 C; 168 G; 110 T; 0 U; 0 Other;
                                                                                     Antibacterial; infection; vaccine; gene therapy; gene; ds.
                                                                  N. gonorrhoeae nucleotide sequence SEQ ID 2509.
                                                                                                                                                                                                                                Monaci E;
                                                                                                                                                                                                                                                                                                              Disclosure; Page 371; 815pp; English
                                                                                                                                                                                                                               Masignani V,
        ABZ38960 standard; DNA; 486 BP
                                                                                                                                                                    12-FEB-2002; 2002WO-IB002069.
                                                                                                                                                                                        12-FEB-2001; 2001GB-00003424.
                                                                                                                                                                                                                               Fontana MR, Pizza M,
                                                                                                          Neisseria gonorrhoeae
                                                                                                                                                                                                                                                  WPI; 2003-058415/05.
                                                                                                                                                                                                           (CHIR-) CHIRON SPA
                                                                                                                                                                                                                                                             P-PSDB; ABP77990
                                                                                                                             WO200279243-A2
                                               07-MAR-2003
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ABZ38960/c
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Search completed: May 19, 2005, 15:25:55 Job time : 1070 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABZ37706-ABZ42016 represent nucleic acid molecules of the invention
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Best Local Similarity 95.6%;
Matches 390; Conservative C
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186 AATGTCGATCTGGATGCCGGCTACCGCTACAACTACGTCGGCAAAGTCAACAATGTCAAA 127
                          478 AACGICCGITCCGGCGAACTGICCGTCGGCGTCGCGCGTCAAATTCTGA 525
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Sequence 5, Appli
Sequence 7, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 2, Appli
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Sequence 1, Appli
Sequence 1, Appli
Sequence 363, Appli
Sequence 363, Appli
Sequence 71, Appli
Sequence 71, Appli
Sequence 1, Appli
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Sequence 15, Appl
Sequence 2, Appli
Sequence 6, Appli
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                                                                                                May 19, 2005, 15:26:04 ; Search time 540 Seconds (without alignments) 1590.825 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
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US-08-913-362-5

US-08-913-362-29

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US-08-913-362-3

US-09-913-912-175

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3 US-09-103-840A-1

US-08-961-527-363

US-09-107-649-7

US-09-107-649-7

US-09-902-540-1169

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US-08-902-540-1169
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                                                                                                                                                                                                                                                                                                 1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                   - nucleic search, using sw model
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95.7 528 3
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8.3 105 3
8.1 36519 3 US
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seq length: 200000000
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Match Length
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42.8
42.4
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Perfect score:
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Maximum DB
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ALIGNMENTS

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UNIVERSILATION OF GRAPES

PRETENT NO. 6287574

PROJECTANT: Brodeur, Bernard R

PROJECTANT: Brodeur, Clement

TITLE OF INVENTION: PROTEINAER RESISTANT SURFACE PROTEIN

TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STRATE: D.C.

STATE: D.C.

CONFUTER: BADABLE FORM:

MEDION TYPE: PLOPEY disk

CONFUTER: BADABLE FORM:

MEDION TYPE: PLOPEY disk

CONFUTER: BADABLE FORM:

SOFTWARE: Patentin Release #1.0, Version #1.30

CONFUTER: BADABLE FORM:

PRINT APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: US 60/001,983

FILING DATE: 04-AUG-1995

ATTORNEY APPLICATION NUMBER: 04/998/0128

FILING DATE: 04-AUG-1995

ATTORNEY APPLICATION NUMBER: 04/998/0128

FRIENCE PREMOKE PREMACHERISTICS:

LENGTH: 810 base pairs

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATICS:

LENGTH: 810 base pairs

TYPE: UNICH CACH CACH

STELEX: 904136

TELEX: 904136

TELEX: 1000 FOR STELEY

TELEX: 1000 FOR STEL
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GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 120
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Pred. No. 3e-136;
0; Mismatches 4; Indels 0
                                                                                       CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERLE, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET UMBER: 29,768
REGISTRATION NUMBER: 29,768
REFERENCE/POCKET UMBER: 29,768
REFERENCE/POCKET UMBER: 29,768
REFERENCE/POCKET UMBER: 29,768
REFERENCE/POCKET UMBER: 29,768
RELEPHONE: (202)672-5399
THELEFAK: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: Neisseria meningitidis STRAIN: Z4063
                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 850 base pairs TYPE: nucleic acid STRANDEDNESS: double TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.8%;
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Best Local Similarity 99.2
Matches 521; Conservative
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LOCATION:
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LOCATION:
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, LOCATION:
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Best Local Similarity 100.0%; Pred. No. 4.8e-138;
Matches 525; Conservative 0; Mismatches 0; Indels
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Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Marcin, Denis
APPLICANT: Marcin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          525
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STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                ORGANISM: Neisseria meningitidis STRAIN: 608B
                                                                                                                                       sig_peptide
143..199
                                                                                                                                                                                                  mat_peptide 200..667
                                                                           CDS
143..667
ORIGINAL SOURCE
                                                      FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                   NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-08-913-362-1
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US-08-913-362-5
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                                                                                                                  FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                               240
                                                                                                                                                                                       GGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGC 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601 AGCAAAACCTCCGCCCGGCCTCCGGCGTATTGGCGGGCGTAAGCTATGCCCGTTACCCCGAAT
                                                                                                                                                                 1 ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
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US-08-913-362-29

US-08-913-362-29

Sequence 29, Application US/08913362

Sequence 29, Application US/08913362

Sequence 29, Application US/08913362

APPLICANT: Brodeur, Bernard R

APPLICANT: Brodeur, Denis

APPLICANT: Rioux, Clement

TILLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN

TILLE OF INVENTION: OP NEISSERIA MENINGITIDIS

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & Lardner

STRET: 3000 K ~ CTTV
                                                                                                                                ö
                                                                                           Length 810;
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                                                                                                                                Indels
                                                                                 ; Pred. No. 9.5e-132; 0; Mismatches 14: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC_compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
                                                                                         95.7%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                             Best_Local Similarity 97.3
Matches 511; Conservative
                 mat_peptide
298..765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Wash
STATE: D.C
                 NAME/KEY:
COCATION:
US-08-913-362-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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FEATURE
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                                                                                                                      GTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAAC 480
                                                        568 AGCCAAACTCCACCGGCCTCGGCGTATTGGCGGGCGTAAGCTATGCCGTTACCCCGAAT 627
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Jose
APPLICANT: Hamel, Jose
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
                                                                                                                                                                                          GTCCGTTCCGGCGAACTGTCCGCCGGTGTGCGCGTCAATTCTGA 732
                                                                                                                                                                       GTCCGTTCCGGCGAACTGTCCGTCGGCGTGCGCGTCAAATTCTGA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLUM LIEL PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 60/001,983
FILING DATE: 17-MAR-1995
APPLICATION NUMBER: US 60/001,983
FILING DATE: OF ANG-1995
APPLICATION NUMBER: 29,768
TRING BAPICATION INFORMATION:
NAMM: BAPICATION NUMBER: 29,768
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 20,768
TELEFAX: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Neisseria gonorrhoeae
STRAIN: b2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPAX: ...
TELEX: 904136
INFORMATION FOR SEO ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 810 base pairs
"vp8: nucleic acid
"vp8: nucleic acid
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241..297
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241..765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
LOCATION:
FEATURE:
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LOCATION:
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                                                                                             421
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61 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCAAAAGCCTCAAGCTCTTTA 120
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TITLE OF INVENTION: DEPOTEINAGE K RESISTANT SURFACE PROTEIN TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS NUMBER OF SEQUENCES: 30 CORRESPONDENCE ADDRESS: ADDRESSE: Foley & Lardner STREET: 3000 K Street, N.W., Suite 500 CITY: Washington STATE: D.C. COUNTRY: USA ZIONER STATE: D.C. COUNTRY: USA ZIONER READABLE FORM: MEDING THE READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.6%; Score 491.2; DB 3; Length 710; 97.0%; Pred. No. 1.5e-128; ive 0; Mismatches 13; Indels 3
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362 FILING DATE: 13-NOV-1997 PRIOR APPLICATION NUMBER: US 08/406,362 FILING DATE: APPLICATION NUMBER: US 08/406,362 FILING DATE: 17-NAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMONIONICATION INFORMATION:
TELEPHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELERS: 904136
; INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 710 base pairs
TUBER: mucleic acid
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MOLECULE TYPE: DNA (genomic)
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
FEATURE:
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FEATURE:
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TICGCCGICCATIACACGCGCIACAAAACIATAAACAAGYCCCAICCACCGATITCAAA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTTACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCCAATCGCCCGTCAAACCG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241 CTTTACAGCATCGGCGCGCCGYCATTTACGACTTCGACACCCAATCSCCCGTCAAACCG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCTCGGCGCGCGCTTGAGCCTCAACCGCCCTCCGTCGACTTGGGCGGCAGCGACAGC 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TICAGCCAAACCICCAICGGCCICGGCGIAITGACGGGCGIAAGCIAIGCCGITACCCCG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               418 AATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAA 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AIGAAAAAGCACTIGCCRCACTGATIGCCCTCGCHCTCCCGGCCGCCGCACTGGGGGAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ATGAAAAAAGCACTTGCCACACTGATTGCCCTCGCTCTCCCGGCCGCCGCACTGGCGGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             478 AACGICCGITCCGGCGAACIGICCGICGGCGIGCGCGTCAAAITCIGA 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 AAYGTCCGTTCCGGCGAACTGTCCGYCGGYGTRCGCGTCAAATTCTGA 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 501.2; DB 3; Length Pred. No. 2e-131; 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.5%; Scor.
95.1%; Pred. No. 2c.
've 22; Mismatches
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
RICH APPLICATION DATA: 0.001,983
FILING DATE: 04-AUG-1995
ATTORNEY, AGENT INFORMATION: 0.001,083
ATTORNEY, AGENT INFORMATION: 0.001,083
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 29,768
TELECOMMUNICATION INFORMATION: TELECHNUM: (202)672-5300
TELEFAX: (202)672-5309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other nucleic acid
/desc = "consensus"
                                                                                                                                                                                                                                                                                          TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                           LENGTH: 528 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.1<sup>3</sup>
Matches 502, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: 11:
MOLECULE TYPE:
DESCRIPTION:
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US-08-913-362-3
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Sequence 3, Application US/08913362
Patent No. 6287574
GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee

176 GGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACGCCAAAGCCTCAAGCTCTTTA 235

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OTHER INFORMATION: CDC 1551

OTHER INFORMATION: "n" bases at various positions throughout the sequence

OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OP INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OP INVENTION: TUBECULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
SURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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44.6%; Pred. No. 0.094;
tive 0; Mismatches 224; Indels 0;
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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LENGTH: 4403765
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49.8%; Pred. No. 0.00035;
iive 0; Mismatches 127; Indels 0
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TITLE OF INVENTION: Plant Metabolism Genes
FILE REFERENCE: BB1378 US NA
CURRENT APPLICATION NUMBER: US/09/614,912
CURRENT FILING DATE: 2000-07-12
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PRIOR PELING DATE: 1999-07-30
PRIOR FILING DATE: 1999-07-30
PRIOR PILING DATE: 1999-12-15
PRIOR APPLICATION NUMBER: 60/170,906
PRIOR FILING DATE: 1999-12-15
PRIOR FILING DATE: 1999-12-15
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PRIOR FILING DATE: 1999-12-21
NUMBER OF SEQ ID NOS: 204
SOFTWARE: Microsoft Office 97
SEQ ID NO 175
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Lee, Jian Ming
Sakai, Hajime
Weng, Zude
Caimi, Perry G
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Rafalski, Antoni
Orozco, Buddy
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APPLICANT:
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LENGTH: 4411529
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SEQ ID NO 2
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Becent No. 6294328

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FRAZER, Claire M.
APPLICANT: WHITE, Owen R.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-22007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2.
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                       APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver. 2.1
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Pred. No. 0.095;
0; Mismatches 224; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                     Application US/09103840A
                                                                   Sequence 1, Application US/091038
Patent No. 6294308
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 44.6%;
Matches 180; Conservative
                                                                                                                                                                        WHITE, Owen R.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
LENGTH: 4411529
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US-09-103-840A-2/c
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                                                                                                                        OTHER INFORMATION: UDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
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APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBRECULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN Ver: 2.1
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Pred. No. 0.14;
0; Mismatches 210; Indels 0;
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Pred. No. 0.14;
0; Mismatches 210; Indels
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LENGTH: 4403765
TYPE: DNA
OKGANISM: Mycobacterium tuberculosis
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Mycobacterium tuberculosis OTHER INFORMATION: H37Rv
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Patent No. 6294328
GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
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Best Local Similarity 44.9%;
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                            Best Local Similarity 44.9
Matches 171; Conservative
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Sequence 363 Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2839 aceaerecriceecricacarcaaceaerecercaecercaecaacaacairca 2898
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2719 Accadrócororgancacarcaacaagecorocecricageaageacacacacages 2778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -CGACTTCGACACCCAATCGCCCGTCAAACCGTATCTCG 304
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102 GCCTCGCCGCGCGCGCGTACCTCATCGGCCTCGACACATCCCGCATCCGCCATCGGC 761
                                                                                                                                                                                                   762 circabasakakaceceredasereseseseresidekaredastresidekakakakadasta 821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 ACACGCGCTACAAAAACTATAAAGCCCCATCCACCGATTTCAAACTTTACAGCATCGGCG
                                                                                                                            Score 44; DB 3; Length 446
Pred. No. 0.021;
0; Mismatches 185; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33 OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEB: Human Genome Sciences, Inc. 1: 9410 Key West Avenue Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY GABNT INFORMATION:
NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCS/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
TELEPAN: (301) 309-8504
TELEPAN: (301) 309-8512
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                      822 CTĆCŤČATĆAAĠĠCĆCTČATĆĠĄĆ 845
                                                                                                                                                                                                                                                                                               331 TCCGTCGACTTGGGCGGCAGCGAC 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 47.3%;
Matches 174; Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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STATE: Maryland
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OTHER INFORMATION: Organophosphate Hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                126733 GECTTCGGCGTCGGCCTATCCGGCGACACCCAGGTGGGCATCGGCGCACCCAACTCGGGC 426574
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                                                                                                                                 426853 AACACCGGTTTCTTCAACTCCGGCACCGCCAACACCGGCTTGTTCAACTCCGGCACCGGC 426794
                                                                                                                                                                                                                                                                                           426793 AACACCGGCTTGTTCAACTCGGGCACCGGCAACGTCGGCATCGGCAACATGGGCACCGGC 426734
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APPLICANT: HOWARD, JOHN
APPLICANT: BAILEY, MICHELE
APPLICANT: GASTEL, FRANS VAN
APPLICANT: GASTEL, FRANS VAN
APPLICANT: WANG, HUAMING
APPLICANT: WARD, MICHAEL
TITLE OF INVENTION: BUZYMES PRODUCED IN PLANTS
FILE REPERBURCE: 1003.2R
FULE REPERBURCE: 1003.2R
CURRENT FILING DATE: 2001-06-14
PRIOR FILING DATE: 2000-06-15
NUMBER OF SEQ ID NOS: 5
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                                                                                                                                                                                                                312
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                                                                                                                                                                                                                                                                                                                                                                              313 TTGAGCCTCAACCGCGCCTCCGTCGACTTGGGCGGCCACGCGACGCTTCAGCCTAAACCTCC 372
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Patent No. 6632930
GENERAL INFORMATION.
APPLICANT: HOOD, ELLEBETH
APPLICANT: HOWARD, JOHN
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ORGANISM: Artificial Sequence
FEATURE:
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Matches 149; Conservative
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SEQ ID NO 4
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FILE REFERENCE: NEXOZ/C1-CON
CURRENT APPLICATION NUMBER: 07/829,461
EARLIER APPLICATION NUMBER: 07/829,461
EARLIER PILING DATE: 1992-01-31
EARLIER FILING DATE: 1991-00-01-31
EARLIER FILING DATE: 1991-00-01-31
EARLIER FILING DATE: 1991-00-01
EARLIER FILING DATE: 1991-00-01
EARLIER FILING DATE: 1991-00-01
EARLIER FILING DATE: 1991-00-02
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 390
                                                                                                                                                                      ATTTGGATGCCGGCTACCGCTACAACTACATCGGCAAAGTCAACACTGTCAAAAACGTCC 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              147 CATCTCCGCAGGCTACCGCATCAACGACCTCCGCTTCGCCGTCGATTACACGCGCTACAA
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Pred. No. 0.011;
0; Mismatches 199; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09197649
Patent No. 6194550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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Best Local Similarity 45.0%;
Matches 163; Conservative
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Patent No. 6420135
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
                                                                    2899 GAATCIGCATCAACCAGTGCGICCGCTTCAGCGICAACCAGTGCGICGGCTTCAGCGICG 2958
                                                                                                                                                                    2959 ACAAGTGCTTCGGCTTCAGCATCAACGAGTGCGTCGGCCTCAGCAAGCGCAAGTACCTCA 3018
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                         365 AAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCGAATGTCG 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   134 GCTTCAGCCCGCGCATCTCCGCAGGCTACCGCATCAACGACCTCCGCTTCGCCGTCGATT 193
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                                                                                                                      425 ATTTGGATGCCGGCTACCCCTACAACTACAACGCAAAGTCAACACGTGAAAAACGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                194 ACACGCGCTACAAAACTATAAAGCCCCATCCACCGATTTCAAACTTTACAGCATCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 9410 Key West Avenue CITY: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Brookes, A. Anders
REGISTRATION NUMBER: 36,373
REFRENCE/DOCKET NUMBER: PB34
TELEPHONE: (301) 309-8512
TRELEPKX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 33768 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 32768 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                 3019 GCGTCAGC 3026
                                                                                                                                                                                                                    485 GTTCCGGC 492
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Best Local Similarity
Matches 174; Conserva
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US-08-961-527-71
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428 TGGATGCCGGCTACCACTACATCGCCAAAGTCAACACTGTCAAAAACGTCCGTT 487
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                                                                                                                    368 CCTCCATCGGCCTCGGCGTATTGACGGGCGTAAGCTATGCCGTTACCCCGAATGTCGATT 427
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APPLICANT: Stassi, Diane L.
APPLICANT: Summers Jr., Richard G.
APPLICANT: Ruan, Xiaoan
APPLICANT: Pereda-Lopez, Ana
APPLICANT: Kakavas, Stephan J.
TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
NUMBER OF SEQUENCES: 34
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/868,003
FILING DATE: 16-MAY-1979
CLASSIFCATION: 435
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Dianne Casuco
REGISTRATION NUMBER: P-40,943
REFERENCE/DOCKET NUMBER: 4952.US.P2
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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100 Abbott Park Rd.
                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08858003
Patent No. 6060234
GENERAL INFORMATION:
APPLICANT: Katz, Leonard
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SEQUENCE CHARACTERISTICS:
LENGTH: 925 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
JOPOLOGY: linear
US-08-858-003-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
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Matches 175; Conserv
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US-08-858-003-1
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CA197724 SCACADD107
CA193415 SCCCFL100
CB654660 OSUNECOTF
CB640993 OSUNECOTF
CV152413 LS245-S.S
CB677411 OSUNEC155
CB677411 OSUNEC165
CB6771800 OSUNEC165
CB6771800 OSUNEC167
CB6771800 OSUNEC17
CB67739 OSUNEC17
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CB668023 OSUNEC17
CB66803 OSUNEC17
CB6803 OSUNEC17
CB68
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5.1.6
Compugen Ltd.
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   GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%
Maximum Match 100% \( \)
Listing first 45 summaries
                                                                                                                           nucleic search, using sw model
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CB64099315
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Gapop 10.0 , Gapext 1.0
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9b est2:;

9b est3:;

9b est4:;

9b est6:;

9b gs81:;

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Match Length
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Perfect score:
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Maximum DB &
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BH898151 MB61p2A7 CD219573 CCC1_55_A CD22538 CCC1_22_G CD222866 CCC1_24_B CB681064 OSJNEF66N CL978445 OSIFCC031 CL978445 OSIFCC031 CL978445 OSIFCC031 CL978445 OSIFCC021 CL971648 OSIFCC021 CL971648 OSIFCC021 CL67625 BJ748832 CL971648 OSIFCC021 CK67632 FGAS05203 BG560157 RHIZ2_71 A189106 GH20192.5 CD223038 CCC1_55 B AN680997 WSI_9=10 BES57605 DG1_21_E0 CD263595 BTHI_45_F CC0250025 AGENCOURT CL974133 OSIFCC042	ALIGNMENTS 622 bp mRNA linear EST 25-SEP-2003	cinarum cona cione hyta; Embryophyta; opsida; Poales; Pc Saccharum; Saccha	, Kemper, E.L. and Arruda, P. 1-7 (2001) r e Engenharia Genetica npinas 0, Campinas SP, Brazil	Tex: 55 19 3788 1089 Email: parruda@unicamp.br Clone distribution: clone distribution information can be found clone distribution: clone distribution at through the Brazilian Clone Collection Center (BCCC) at http://www.bcccenter.fcav.unesp.br Plate: 074 row: C column: 04 Seq primer: T7 Promoter Primer. Location/Qualifiers 1. 622 /crganian="Saccharum officinarum" /mol_type="mRNA"	/clone="SCAGADJ074C04" /clone="SCAGADJ074C04" /lab_host="DHJ08" /lab_host="DHJ08" /lab_host="DHJ08" /locine lib="ADJ" /note="Organ: Seedlings inoculated with Gluconacetobacter diazotroficans; Vector: pSport1; Site_1: Sal1; Site_2: /note="Organ: Seedlings inoculated from library generated from fseedlings inoculated with Gluconacetobacter diazotroficans]. ONA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The Gluble-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details
BH898151 CD219573 CD222538 CD222866 CB681064 CL973983 BJ748832 CL971648 CL971648 CL971648 CL971648 CCB643751 CK167632 CCB643595 CD250025 CCB688257	ALIGNMENTS	sccna 59 tae; iophy ndrog	complex. 1 (bases 1 to 622) Vettore, A.L., da Silva, F.R., Ken The libraries that made SUCEST Genet. Mol. Biol. 24 (1-4), 1-7 Contact. Arruda P Centro de Biologia Molecular e E Universidade Estadual de Campine Caixa Postal 6010, 13083-970, Ce	ax: 55 19 3788 113/ mail: parruda@unicamp.br lone distribution: clone distribution: olone distribution; olone to trp://www.bcccenter.fcav.unes) late: 074 row: C column: 04 eq primer: T7 Promoter Primer Location/Qualifiers 1. 622 /organism="Saccharum of column"/mol_trpe="mRNA"	/db xref="texon.4547" /clone="ScAGAD1074C04" /lab_host="PH108" /clone lib="Ab1" /note="Organ: seedlings diazotroficans; Vector: Not1; An unidirectional [seedlings inoculated wideacotroficans]. CDNA was SuperScript Plasmid System CL-2B 40cm-columns and it. 5 Kb were directional].
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Spermatophyta, Magnollophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Saccharum, Saccharum officinarum
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Plate: 003 row: E column: 05
Seq primer: T7 Promoter Primer.
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of each source of RNA and library construction can b obtained at http://sucest.lad.ic.unicamp.br/public"
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                                                                                                                                             Length 622;
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Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
                                                                                                                                      Score 57.8; DB 6; Length.6 Pred. No. 4.3e-05; 0; Mismatches 192; Indels
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/db_xref="taxon:4547"
/clone="SCCCFL1003E05"
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COMMENT

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Oryza sativa (japonica cultivar-group)

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantee; Streptophyta; Embryophyta; Tracheophyta;

Epthartoidae; Oryzae; Oryzae; Oryzae; Datasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.

Large-scale identification of ESTs involved in the interaction

between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute
University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA
/clone_lib="Fpl"
/note="Organ: Inflorescence at begining of development
/note="Organ: Inflorescence at begining of development
(lam-long), Vector: pSport1; Site_1: Sal1; Site_2: Not1;
An unidirectional cDNA library generated from
[Inflorescence at begining of development (lcm-long)].
CDNA was prepared from polyA+ mRNA using SuperScript
Plasmid System Kit (Invitrogen). The double-strand cDNAs
were fractionated in a sepharose CL-2B 40cm-columns and
fragments sizing between 0.8 and 1.5 Kb were
directionally cloned into the vector. Details of each
source of RNA and library construction can be obtained at
http://sucest.lad.ic.unicamp.br/public"
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llarity 47.2%; Pred. No. 0.00011;
Conservative 0; Mismatches 191;
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Tel: 520 626 3967
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hes 171; Conserv
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Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Site_2:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460
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/note="Vector: pBluescript II KS +; Site 1: EcoRI; {
**Not; 6 hrs after innoculation with Rice Blast (Che 86061)*
                                                                                                                                                                                                                                                                                                                                                                                           ΑZ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponbare"
/db xref= txon: 39947"
/clone="OSJNEA17P21"
                                                                                                                                                                                                                                                                                                                                                                                           Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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Pred. No. 0.00063;
0; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                    Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088,
85721-0088, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FORWARD: atc agc ggc cgc gat cc
BACKWARD: aat taa ccc tca cta aag gg
Plate: 17 row: F column: 21
Seq primer: atc agc ggc cgc gat cc.
Location/Qualifiers
                                                                                                                                          between rice and Magnaporthe grisea
Unpublished (2003)
Contact: Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 520 621 9288
Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="Leaf"
/dev_stage="3_week"
/lab_host="DH108"
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Best Local Similarity 44.5%;
Matches 212; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 520 626 3967
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 6 hrs after innoculation with Rice_Blast (C9240-1)"
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, Ehrhartoideae, Oryzeae, Oryza.
1 (bases 1 to 591)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 TCCCCGTCGACAACAACAACAACAAGAGTCCTACGGCGGCGCCGCCAAGATCAACAACA
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/organism="Oryza sativa (japonica cultivar-group)"
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Pred. No. 0.00023;
0; Mismatches 263; Indels
                                                                                                                                                                                      BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: F column: 21
Seq primer: gta aaa cga ccg gcc gtg.
Location/Qualifiers
                                                      http://genome.arizona.edu
                                                                                                                                                   FORWARD: gta aaa cga cga gtg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:39947"
/clone="OSJNEc07F21"
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/cultivar="Nipponbare"
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/lab_host="DH10B"
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Isolation and chromosomal mapping of the rice clones differentially induced under abiotic stress conditions
Unpublished (2004)
Contact: Lee Jung-Sook
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/tissue_type="Leaf"
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/dev_tagge="one weef"
/clone lib="Cold stressed rice cDNA library"
/note="Vector: pBluescript SK+; Cold treatment by placing at 40C for 16 hour after growth on MS medium for one week"
               EST 08-SEP-2004
CV152413
LS245-S.SEQ Cold stressed rice cDNA library Oryza sativa (japonica cultivar-group) cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
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Pred. No. 0.00063;
0; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                                                   Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tal: 82 31 299 1663
Fax: 82 31 299 178
Fax: 82 31 299 178
Email: jungsle@crda.go.kr.
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/cultivar="Ilpumbyeo"
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EST 09-APR-2003
                                                                                                                                                                                           Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases I to 690)
Jantasuriyarat, C., Lu, Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Unpublished (2001)
Contact: Rod Wing
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/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCCGCGCGTTCTCCGCAGGCT 160
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                                  OSJNEC05A17.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA clone OSJNEC05A17 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 698
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Il Similarity 44.5%; Pred. No. 0.00064;
212; Conservative 0; Mismatches 264;
   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 05 row: A column: 17
Seg primer: gta aaa cga cgg cca gtg.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
dq 869
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/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db xref="taxon:39947"
/clone="OSJNEC05A17"
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/dev_stage="3 week"
/lab_host="DH10B"
                                                                                                                                 CB653730.1 GI:29657455
EST.
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/tissue_type="Seedling leaves"
/dev_stage="16-day-old rice seedling treated by JA/BTH"
/clone_lib="Subtracted cDNA library of JA/BTH-treated rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-SEP-2003
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzae; Oryza.

1 (bases 1 to 741)
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/cultivar="Drew (a major cultivated variety in Arkansas)"
/db xref="taxon:3947"
/clone="UB193"
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                                                                                                                                                                                                                                                                                                        262 TCGGCTCCGGCAAGCTCGCCTTCGGCGCCCAAGGCCGACCGCTACAACAGCGTCAACC 321
       142 ACCGCCGCAACGAGCCGGCCTTCGACGCGAGTACCACCACTTCTCCTCCCCCCTCCCCCG 201
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                                                                                                                                                        ccaagaacgccarcgccaacarcaacgccgcgrcgcgaaaccrggarggcccggccrca
                                                                                     221 CATCCACCGATTTCAAACTTTACAGCATCGGCGCGTCCGCCATTTACGACTTCGACACCC
                                                                                                                                                                                                                                  281 AATCGCCCGTCAAACCGTATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       401 GCTATGCCGTTACCCCGAATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 382 ACAACGTCAACGCCTTCGGGTTCAACAAGATGGGGGGTTACAACAACAGCAGCAGCAACGGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subtracted cDNA library of JA/BTH-treated rice leaf
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217 Plant Sci Bldg, Fayetteville, AR 72701,
Tel: 501-575-5635
Fax: 501 575 7601
Email: yiyang@uark.edu
Seg primer: T7
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1. .741
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Contact: Yinong Yang
Plant Pathology Department
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CB677411 725 bp mRNA linear EST 09-APR-2003 OSJNEe14E24.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA clone OSJNEe14E24 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oriza sativa (japonica cultivar-group)
Bukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Varidiplantae; Streptophyta; Encouples; Poaceae;
Bhrhartoideae; Oryzeae; Oryzea.
1 (bases I to 725)
1 (bases I to 725)
2 (Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone lib="OSJNEs"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
KhoI; 24 hrs after innoculation with Rice Blast (70-15)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCGCATCAACGACCTCCGCTTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCC 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGCCGCCGCCGCACTGGCGGAAGGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACG 100
347 TCCCGTCGACAACAACAACAAGTCCTACGGCGGCGCCCCAAGATCAACAACA 406
                                                                                                                     401 GCTATGCCGTTACCCCGAATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCA 460
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                                                                                                                                                                                                                                                                                                                                           167 GCGGCAACTACGGCGGCGACGGGGGCGGAGGCTACTTCAACAAGTCGGTC 522
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/mol type="mRNA"
/cultivar="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 53.6; DB 6; Length 72
Pred. No. 0.00064;
0; Mismatches 264; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group)
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BACKWARD: gga aac agc tat gac cat g
Plate: 14 row: E column: 24
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db xref="taxon:39947"
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/dev_stage="3 week"
/lab_host="DH108"
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Tel: 520 626 3967
Fax: 520 621 9288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Rod Wing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1, .725
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AUTHORS
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COMMENT
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762 bp mRNA linear EST 09-APR-2003
OSJNEE14C19.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA
Clone OSJNEE14C19 5', mRNA sequence.
CB677339
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Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bhrhartoideae; Oryzaa.
1 (Bases I to 762)
1 (Bases I to 763)
1 (Bases I to 763)
1 (Contact: Rod Wing
                                  /note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2: XhoI; 24 hrs after innoculation with Rice Blast (70-15)"
                                                                                                                                                                                                                                                                                                                                  CGGCCGCCGCCGCACTGCCGAAGGCGCATCCGGCTTTTACGTCCAAGCCGATGCCGCACACG 100
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                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                    Length 759;
                                                                                                                                                                            Score 53.6; DB 6; Length 7
Pred. No. 0.00065;
0; Mismatches 264; Indels
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BACKWARD: gga aac agc tat gac cat
Plate: 14 row: C column: 19
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Fax: 520 621 9288
Email: http://genome.arizona.edu
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University of Arizona
Biological Sciences West, 448A,
   /clone_lib="OSJNEe"
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                                                                                                                                                                                                                       Similarity
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Matches 212
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Jantasuriyazat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Jantasuriyazat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E.,
Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction
between rice and Magnaporthe grisea
Compublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 09-APR-2003
CAGCAGCGGCCATGGAGGGATACGACCGCGAGTTCTACCAGTTCAGCGACCAGCTGCGGC 118
                                                                                                                                              119 TGCAGACGGCGAGCTTCTCCGGCCTCTCCCTCGCGACTCCATCTGGTCCTCCCCTCCG 178
                                                                                                                                                                                                                   161 ACCGCATCAACGACCTCCGCTTCGCCGTCGATTACACGCGCTACAAAACTATAAAGCCC 220
                                                                                                                                                                                                                                                             221 CATCCACCGATTTCAAACTTTACAGCATCGGCGGTCCGCCATTTACGACTTCGACACCC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                          239 CCAAGAACGCCATCGCCAACATCAACGGCGTCGCCGGAAACCTGGATGGCCCGGGCCTCA 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   281 AATCGCCCGTCAAACCGTATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        299 TCGGCTCCGGCAAGCTCGCCTTCGGCGCCACCAAGGCCGACCGCTACAACAGCGTCAACC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     341 TGGGCGGCAGCGACAGCTTCAGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAA 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 TCCCCGTCGACAACAACAACAACAAGTCCTACGGCGGCGCCGCCAAGATCAACAACA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    401 GCTATGCCGTTACCCCGAATGTCGATTTGGATGCCGGCTACGCTACAACTACATCGGCA 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             419 ACAACGTCAACGCCTTCGGGTTCAACAAGATGGGGGGTTACAACAACAGCAGCAGCAACGGCG 478
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Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CB671800 759 bp mRNA linear EST 09-APR-20 OSJNEe05117.f OSJNEe Oryza sativa (japonica cultivar-group) cDNA clone OSJNEe05117 5', mRNA sequence.
                                                                         CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 AAGTCAACACTGTCAAAAACGTCCGTTCCGGCGAACTGTCCGTCGCGCGTGCGCGTC 516
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
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Biological Sciences West, 448A, P.O. Box 210088, Tucson,
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Location/Qualifiers
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BACKWARD: gga aac agc tat gac cat
Plate: 05 row: I column: 17
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/clone="OSJNEe05117"
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/dev_stage="3 week"
/lab_host="DH108"
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Fax: 520 621 9288
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Oryza sativa (japonica cultivar-group)
      Arizona Genomics Institute
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Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhattoideae; Oryzaee; Oryzae.
1 (bases 1 to 775)
Jantasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.
Large-scale identification of ESTs involved in the interaction Unpublished (2003)
                                                                                                                                                                                                                                                                       /dev_stage="13 week"
/lab_host="DH10B"
/loome_lib="OSJNBS"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
KhoI; 24 hrs after innoculation with Rice_Blast (70-15)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      393 ACAACGTCAACGCCTTCGGGTTCAACAAGATGGGGGGTTACAACAACAGCAGCAACGGGG 452
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    762
/organism="Oryza sativa (japonica cultivar-group)"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 53.6; DB 6; Length 762;
Pred. No. 0.00065;
0; Mismatches 264; Indels
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                                                                                                                   /mol_type="mRNA"
cultivar="Nipponbare"
db_xref="txxon:39947"
clone="0SJNBel4C19"
tissue_type="Leaf"
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/organism="Oryza sativa (japonica cultivar-group)"
/mol type="mRNA"
/cultivar="Nipponbare"
                                                                 ΑZ
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson,
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FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 13 row: K column: 18
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                              85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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/clone="OSJNEe13K18"
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Oryza sativa (japonica cultivar-group)

ORGANISM

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BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: F column: 07
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEd11F07"
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/lab_host="DH10B"
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Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzae.

Ehrhartoideae; Oryzae; Oryza.

(batasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E., Kudra, D., Dean, R., Soderlund, C., Wing, R. and Wang, G. Large-scale identification of ESTs involved in the interaction Unpublished (2003)
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/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after innoculation with Rice Blast (C9240-1)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 CAAAAGCCTCAAGCTCTTTAGGTTCTGCCAAAGGCTTCAGCCCGCGCATCTCCGCAGGCT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                108 rgcAgAcGGcGAGCTrcrccGGCCrcrccCcrcGcGACrcCArcrGGrcCrcCCCCCCC 167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     168 ACCGCCGCAACGAGCCGGCCTTCGACGGCGAGTACCACCACTTCTCCTCCCCCCTCCCCCG 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCCACCGATTTCAAACTTTACAGCATCGGCGCGGTCCGCCATTTACGACTTCGACACCC 280
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Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
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Pred. No. 0.00065;
0; Mismatches 264; Indels
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BACKWARD: gga aac agc tat gac cat g
Plate: 07 row: G column: 20
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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/cultivar="Nipponbare"
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/dev_stage="3 week"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                     Contact: Rod Wing
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COMMENT
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OSJNEd11F07.f OSJNEd Oryza sativa (japonica cultivar-group) cDNA clone OSJNEd11F07 5', mRNA sequence.
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
Xho1; 24 hrs after innoculation with Rice Blast (C9240-1)"
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Buhartoideae; Oryzeae; Oryza.
1 (bases I to 782)
Jantasuriyarat, C., Lu, G., Gowda, M., Hatfield, J., Zhou, B., Mazur, E.,
Kudrna, D., Dean, R., Soderlund, C., Wing, R. and Wang, G.
Large-scale identification of ESTs involved in the interaction
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 217
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
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/organism="Oryza sativa (japonica cultivar-group)"
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Larity 44.5%; Pred. No. 0.00065;
Conservative 0; Mismatches 264; Indels
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CF278525 S61 bp mRNA linear EST 14-AUG-2003 14ETL--04-H12.bl Rice etiolated leaf plasmid cDNA library (14ETL) Oryza sativa (japonica cultivar-group) cDNA clone 14ETL--04-H12, CF278525
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Oryza sativa (japonica cultivar-group)
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sukaryota; Wiridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzeae; Oryza.
I (bases I to 56.1)
I (bases I to 56.1)
Song, S. I., Kim, J. K., Kim, M. J., Lee, T. H., Shin, Y. C.,
Large-scale Sequencing Analysis of Rice ESTs
Unpublished (2003)
Contact: Nahm B. H.
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281 AATCGCCCGTCAAACCGTATCTCGGCGCGCGCTTGAGCCTCAACCGCGCCTCCGTCGACT 340
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                                                                                                                                   222 ccaagaaceccarceccaacarcaacececerceccegaaaccreeareecceeeccrea 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                               402 ACAACGTCAACGCCTTCGGGTTCAACAAGATGGGGGGTTACAACAACAGCAGCAACGGCG 461
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                                                                                                                                                                                                                                                                                                     341 TGGGCGGCAGCGACAGCTTCAGCCAAACCTCCATCGGCCTCGGCGTATTGACGGGCGTAA
                                                                                                                                                                                                                                                                                                                                                                                                          401 GCTATGCCGTTACCCCGAATGTCGATTTGGATGCCGGCTACCGCTACAACTACATCGGCA
                                                                                   CATCCACCGATTTCAAACTTTACAGCATCGGCGCTCCGCCATTTACGACTTCGACACCC
                                                                                                                                                                                                                                                                                                                                               342 TCCCCGTCGACAACAACAACAACAAGTCCTACGGCGGCGCCGCCAAGATCAACAACA
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Location/Qualifiers
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/lab_hos=="B.coli DH108"
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Best Local Similarity 44.6
Matches 210; Conservative
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DEFINITION
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ORGANISM
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JOURNAL
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Eukaryora, Viridiplantae; Eureptophyta; Embryophyta; Tracheophyta; Bukaryora; Viridiplantae; Erreptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Enthartoideae; Oryzeae; Oryza.

Santasuriyarat,C., Lu,G., Gowda,M., Hatfield,J., Zhou,B., Mazur,E., Kudrna,D., Dean,R., Soderlund,C., Wing,R. and Wang,G.

Large-scale identification of ESTs involved in the interaction between rice and Magnaporthe grisea

Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute
University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

Est: 520 621 9288

Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                    CB668023 842 bp mRNA linear EST 09-APR-2003 OSJNEG15K14.f OSJNEG Oryza sativa (japonica cultivar-group) cDNA clone OSJNEG15K14 5', mRNA sequence.
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/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; 24 hrs after innoculation with Rice Blast (C9240-1)"
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEG15K14"
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Pred. No. 0.00065;
0; Mismatches 264; Indels
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BACKWARD: gga aac agc tat gac cat g
Plate: 15 row: K column: 14
Seq primer: gta aaa cga cgg cca gtg.
Location/Qualifiers
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/dev_stage="3 week"
/lab_host="DH108"
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AUTHORS
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SOURCE
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Search completed: May 19, 2005, 19:31:26 Job time: 7711 secs

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version 5.1.6
- 2005 Compugen Ltd.
    GenCore
Copyright (c) 1993
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OM protein - protein search, using sw model

May 19, 2005, 19:34:43 ; Search time 302 Seconds (without alignments) 222.835 Million cell updates/sec Run on:

US-10-650-123-2 868 Title: Perfect score:

1 MKKALATLIALALPAAALAE........vntvknvrsgelsvgvrvkf 174 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2105692 seqs, 386760381 residues Searched:

2105692 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A_Geneseq_16Dec04:* 1: geneseqp1980s:* 2: geneseqp1990s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

•	Description	Aaw04891 Proteinas	Abu79079 N. mening	Adf43316 N. mening	Adl16114 Neisseria	Adl13428 Neisseria	Adl24352 N meningi	Adp08236 Neisseria	Adl24383 N meningi	Aaw04893 Proteinas	Aaw04894 Proteinas	Abg91063 Neisseria	Aaw04892 Proteinas	Adl24385 N meningi	Abp77991 N. gonorr	z	Adl24386 N meningi		Adl13426 Neisseria	Adl24384 N meningi	Adl24388 N meningi	Adl24389 N meningi	Aao17579 M catarrh	Abp79561 N. gonorr	Aau97605 Haemophil	Aau97603 Haemophil
	ID	AAW04891	ABU79079	ADF43316	ADL16114	ADL13428	ADL24352	ADP08236	ADL24383	AAW04893	AAW04894	ABG91063	AAW04892	ADL24385	ABP77991	ADL24387	ADL24386	AAB19895	ADL13426	ADL24384	ADL24388	ADL24389	AA017579	ABP79561	AAU97605	AAU97603
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æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	99.5	98.7	98.4	95.0	95.0	95.0	94.5	93.3	91.5	91.4	90.4	90.0	89.8	85.9	75.7	27.0	25.8	25.5	25.5
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Aau97602 Haemophil Aau97604 Haemophil Abp79854 N. gonorr	Abp79754 N. gonorr Aau97601 Haemophil Abp80738 N. gonorr	Abp80098 N. gonorr Abp77624 N. gonorr	ADP80862 N. GONOII ADP80428 N. GONOII ADP77612 N. GONOII	żżż			Adp08324 Neisseria Adt05699 Haemophil
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ALIGNMENTS

Proteinase K resistant N. meningitidis 22 kD surface protein. antibody; detection; probe; surface protein. AAW04891 standard; protein; 174 AA. (revised)
(first entry) 16-OCT-2003 22-DEC-1996 AAW04891; RESULT 1 AAW04891

Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae;

Neisseria meningitidis; strain 608B.

Location/Qualifiers 1. .19 /label= sig_peptide 20. .174 /label= mat_protein 96WO-CA000157. WO9629412-A1. 15-MAR-1996; 26-SEP-1996 Peptide Protein

95US-00406362. 95US-0001983P. 04-AUG-1995;

17-MAR-1995;

(IAFB-) IAF BIO VAC INC.

Martin D, Hamel J, Rioux C;

Brodeur BR,

WPI; 1996-443187/44. N-PSDB; AAT39039. Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, diagnosis of, N. meningitidis infection.

or

Claim 7; Fig 1; 117pp; English.

A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in

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humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
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                                                                                                                                                                                     Length 174;
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                                                                                                                                                                                  100.0%; Score 868; DB 2; 100.0%; Pred. No. 9.3e-87;
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ABU79079 standard; protein; 174 AA (first entry) 18-JUN-2003 ABU79079; RESULT 2

meningitidis lipopolysaccharide protein.

Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis; gene therapy, mammalian cell receptor; cytostatic; tumour associated lipid; anergy; T cell; antigen presenting cell; APC; tumouricidal immunocyte; antitumour.

Neiserria meningitidis.

US2002177551-A1.

28-NOV-2002

30-MAY-2001; 2001US-00870759

31-MAY-2000; 2000US-0208128P

(TERM/) TERMAN D S.

Terman DS;

WPI; 2003-361759/34.

N-PSDB; ACA64711

A mammalian cell receptor, useful in the treatment of cancer by binding to tumor associated lipids where the binding induces anergy or apoptosis cells and antigen presenting cells.

Disclosure; Page; 167pp; English

The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,

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castly actors of grants. Inopepticate and proceoglycolipus are inactivated or deleted), a construct useful in the treatment of cancer comprising a useful in the treatment of cancer (where an adaptor protein which useful in the treatment of cancer (where an adaptor protein which the useful in the treatment of cancer (which is a composition useful in the treatment of functionally deactivated), a composition are all adaptor protein which cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids are inactivated or deleted to produce a tumouricidal lipids are inactivated or deleted to produce a tumouricidal lipids are inactivated or deleted to produce a tumouricidally activated population, and administering the tumouricidally activated or deleted to produce a tumouricidally activated population, and administering AFCs to the host), producing (M3) a tumouricidally contact AFCs, in which adaptor proteins, which inhibit T cells and administering the tumouricidally activated T cells, in which adaptor proteins, which inhibit T cells activated to produce a tumouricidal population of T cells, in which adaptor proteins, which inhibit T cells activated to produce a tumouricidally activated T cells to the host), reating deministering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells to the host, or administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact immunocytes in vivo, producing (M5) a tumour associated antigen to contact immunocytes in which adaptor before the uncoursicidal T cell population in vivo in a mammal (by administering a lipid and antigen accident immunocytes in which adaptor to contact immunocytes in which adaptor contact immunocytes in which adaptor contact immunocytes in which adaptor are deleted or functionally deactivated) and producing or proteins which inhibit T cell population 
sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              was obtained in electronic format from the US patnet "seqdata.uspto.gov/sequence.html?DocID=20020177551"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or incorporated into a fusion construct with a superantigen. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US parnet office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"
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ö Length 174; Indels Query Match 100.0%; Score 868; DB 6; Best Local Similarity 100.0%; Pred. No. 9.3e-87; Matches 174; Conservative 0; Mismatches 0;

Sequence 174 AA;

120 09 1 MKKALATLIALALPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR ò 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120 121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174 셤 셤 ઠે

121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174

ADF43316 standard; protein; 174 AA

12-FEB-2004 (first entry)

receptor; lipid-based tumour associated antigen; cytostatic; antimicrobial; gene therapy; neoplastic disease; tumour; cancer; infectious disease; lipopolysaccharide; LPS.

RESULT 3

ADF43316;

N. meningitidis lipopolysaccharide seq id 36

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30-AUG-2002; 2002GB-00020194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.
Best Local Similarity 100.
Matches 174; Conservative
                                                      Serruto D,
                                                                               WPI; 2004-239124/22
                          (CHIR ) CHIRON SRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 174 AA;
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                                                                                                                                                  detergent
                                                      Pizza M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
ADL13428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                         The invention describes a receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumour associated antigen. The receptor has cytostatic and antimicrobial properties and is suitable for use in gene therapy. The receptors, methods and compositions are useful for treating a neoplastic disease or tumour (cancer), and infectious diseases. This is the amino acid sequence of Neisseria meningitidis lipopolysaccharide (LPS) to which tumour cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                             New receptor in a mammalian cell that inhibits regular activation by receptors specific for lipid-based tumor associated antigens, useful treating a neoplastic disease or tumor, and infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 868; DB 7; Length 174; 100.0%; Pred. No. 9.3e-87; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Outer membrane vesicle preparation, OMV, detergent-free, physical disruption; vaccine; serogroup B; NspA; Neisserial surface protein A; immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis NspA for use in vaccine.
                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 36; 151pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL16114 standard; protein; 174 AA
                                                                               28-DEC-2000; 2000US-00751708.
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Best Local Similarity 100.
Matches 174; Conservative
 Neisseria meningitidis.
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                                                                                                                                                                                       2003-787326/74.
                                                                                                                                  (TERM/) TERMAN D S
                                                                                                                                                                                                     N-PSDB; ADF43315
                                                                                                                                                                                                                                                                                                                                                                                                         develop immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 174 AA;
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                           US2003157113-A1.
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                                                                                                        28-DEC-1999;
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                                                    21-AUG-2003
                                                                                                                                                             Terman DS;
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g 8

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The invention relates to a process for producing an outer membrane vesicle (OWV) preparation from a bacterium. The process involves disrupting the bacterial membrane substantially in the absence of decoxycholate detergent or other detergent, followed by several centrifugation steps. Membrane disruption is achieveded by several homogenisation, microfluidisation, cavitation, osmotic shock, grinding, French press, belnding or any other physical technique. The outer membrane vesicles can be prepared from bacteria of the genera Moraxella, Shigella, Pseudomonas, Treponema, Porphyromonas, Helicobacter or Nisseria, and are particularly produced from Neisseria meningitidis (especially serogroup B) or Neisseria gonorrhoeae. The invention also relates to a Neisseria meningitidis outer membrane vesicle composition in which the vesicles include the immunogens NSPA (Neisserial surface
                                                                                                                                                            Producing an outer membrane vesicle (OMV) preparation from a bacterium, useful as a vaccine against Neisseria meningitidis serogroup B, comprises disrupting the bacterial membrane in the absence of deoxycholate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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100.0%; Pred. No. 9.3e-87;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 20pp; English.
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Rappuoli
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Section 1

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us-10-650-123-2.rag

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The invention relates to an isolated reloided Neisserial surface procein alvention relates to an insolated reloided Neisserial surface procein invention also relates to the method of refolding an NspA protein; an alkaline refolding buffer comprising ethanolamine and SB-12 (3-carrier and optionally one or more other Neisserial antigens; a method of preventing or treating a Neisserial infection; an antigens; a method of preventing or treating a Neisserial infection. NspA has conserved in indicate that it is a potential vaccine candidate for the Aspa protein; and diagnosing a Neisserial infection. NspA has consecuted indicate that it is a potential vaccine candidate for the development of subunit vaccines for the treatment of infections caused by Neisseria meningitidis (meningococcus), which causes invasive bacterarial diseases such as bacteraemia and meningitis, or Neisseria condocred by Neisseria meningitidis (maningococcus), which causes invasive bacterarial diseases such as bacteraemia and meningition and it could consorthoea, the causative agent of gonorrhoea. Recombinantly produced proteins are also be used in the development of new antimicrobial agents, diagnostic tests and in drug screening. However, recombinantly produced proteins are frequently unable to adopt their biologically active conformations, and yields may be very low due to mis-folding and aggregation of the protein. The method of the invention provides an improved method for refolding the protein form partly purified inclusion bodies in amounts up to 100% without the need for further purification. The refolded Neph protein is useful for preparing a composition for diagnosing, treating or preventing infection caused by Neisseria meningitidis or Neisseria gonorrhoeae. The meningitidis H44/76.
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                                                                                                       /note= "The corresponding residue in the mature protein shown in Fig 2 (residue 149) is Ala"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention relates to an isolated refolded Neisserial surface properties of Maintenant monorphoeae. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New refolded NspA protein, useful for preparing a composition for
diagnosing, treating or preventing infection caused by Neisseria
meningitidis or Neisseria gonorrheae.
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                                                                                                                                                                                                                                                                                                                                                                                                           Goraj K, Poolman J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 868; DB 8;
Pred. No. 9.3e-87;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                           Feron C,
1. .19
/label= Signal_peptide
20. .174
/label= Mature_NspA
                                                                                                                                                                                                                                                                                                                                           (GLAX ) GLAXOSMITHKLINE BIOLOGICALS SA. (UYUT-) RIJKSUNIV UTRECHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 3; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                           Denoel P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
100.0%;
                                                                                                                                                                                                                                                         28-AUG-2003; 2003WO-EP010085
                                                                                                                                                                                                                                                                                                   30-AUG-2002; 2002GB-00020197
                                                                                                                                                                                                                                                                                                                                                                                                         Bos M, Denoe, Weynants V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 174; Conservative
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                                                                                   Misc-difference
                                                                                                                                                                          WO2004020452-A2
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  Peptide
                                            Protein
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The present invention relates to a pharmaceutical composition comprising a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608b, where the polypeptide is the NspA protein. The composition is useful for inducing an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection and for treating and/or preventing neisserial infection chosen from N. meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharea. It is useful for treatment or prophylaxis of meningitia and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is the Neisseria meningitidis strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                    121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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100.0%; Pred. No. 9.3e-87;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                          NspA; vaccine; antibacterial; meningitis
                                                                                                                                                                                                                                      N meningitidis strain 608B NspA protein.
                                                                                                                           ADL24352 standard; protein; 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2003; 2003WO-CA001452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-2002; 2002US-0406980P.
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 174; Conservative
                                                                                                                                                                                                                                                                                                              Neisseria meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2004-239123/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Martin D, Rioux S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           608B NspA protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; ADL24351
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                                                                                                                                                                                                                                                                                                                                                 WO2004019976-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 meningitidis.
                                                                                                                                                                                                    03-JUN-2004
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                                                                                                                                                                ADL24352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                          ADL24352
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RESULT

ADL24383;

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The invention relates to a novel composition comprising outer-membrane vesicles (OWV) prepared from a first strain of Neisseria meningitidis and 1 or more proteins which are present in OWVs prepared from a second strain of N. meningitidis, but which are not present in OWVs prepared from the first strain. The composition of the invention demonstrates antibacterial and antihilammatory activities and may be useful in the field of meningococcal biochemistry, in particular the trafficking and localisation of meningococcal infections, as well as in the prevention or treatment of meningococcal infections, possibly via the production of a vaccine or gene therapy. The current sequence is that of a Neisseria meningitidis MCSB outer-membrane vesicle (OWV)-related membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New compositions having outer-membrane vesicles and proteins from Neisseria meningitidis, useful in the field of meningococcal blochemistry, in particular for preventing and/or treating meningococcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                                                                                             Neißseria meningitidis MC58 OMV-related membrane protein - SEQ ID 69.
                                                                                                                                                                                                                                                                                                                                         meningococcal protein trafficking; localisation; infection; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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Pred. No. 2.5e-86;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                outer-membrane vesicle; antibacterial; antiinflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; SEQ ID NO 69; 79pp; English.
                                      ADP08236 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2002; 2002GB-00026734.
27-MAR-2003; 2003GB-00007131.
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Best Local Similarity 99.4%;
Matches 173; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-NOV-2003; 2003WO-IB006281
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis MC58
                                                                                                                                                                          26-AUG-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Norais N, Grandi G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-420615/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHIR ) CHIRON SRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the invention
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ADPO8236

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Composition comprising liposome associated with isolated polypeptide or polymoralectide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N. meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKALATLIALALPAPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 174;
                                                                                                                                                                                                                             'note= "wild-type Gly substituted by Ala"
                                                                                                                                                                                                                                                              /note= "wild-type Asp substituted by Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                    mutein; mutant; NspA; vaccine; antibacterial; meningitis.
                                                                 N meningitidis strain 608B modified NspA protein #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 857; DB 8;
Pred. No. 1.5e-85;
1; Mismatches 1
                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Page; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                      29-AUG-2003; 2003WO-CA001452.
                                                                                                                                                                                                                                                                                                                                                                                                       30-AUG-2002; 2002US-0406980P.
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                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 98.7
Best Local Similarity 98.9
Matches 172; Conservative
                                                                                                                                       Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-239123/22.
                                                                                                                                                                                                          Misc-difference 115
                                                                                                                                                                                                                                               Misc-difference 118
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                                                                                                                                                                                                                                                                                                  WO2004019976-A2
                                  03-JUN-2004
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                                                                                                                                                       Synthetic.
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RESULT 9 AAW04893

ADL24383 standard; protein; 174 AA

ADL24383 ID ADL2 XX RESULT 8

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AAW04894 standard; protein; 174 AA
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                                                                                                                                                                                                                                                                    15-MAR-1996;
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04-AUG-1995;
                                           16-OCT-2003
22-DEC-1996
                                                                                                                                                                                                                                                                                                                           (IAFB-) IAF
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                      AAW04894;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigents of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, or diagnosis of, N. meningitidis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                 Proteinase K reistant, Neisseria meningitidis; Neisseria gonorrhoeae;
antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                             Proteinase K resistant N. meningitidis 22 kD surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 98.4%; Score 854; DB 2; Length 174; Best Local Similarity 98.3%; Pred. No. 3.2e-85; Matches 171; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                 Rioux C;
                                                                                                                                                                  1. 19
/label= sig_peptide
20. 174
/label= mat_protein
                                                                                                                                  Neisseria meningitidis; strain Z4063
                                                                                                                                                         Location/Qualifiers
 AAW04893 standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                 Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 7; Fig 9; 117pp; English.
                                                                                                                                                                                                                                                                     96WO-CA000157
                                                                                                                                                                                                                                                                                          95US-00406362
95US-0001983P
                                                        (first entry)
                                                                                                                                                                                                                                                                                                                           (IAFB-) IAF BIO VAC INC
                                                                                                                                                                                                                                                                                                                                                 Martin D,
                                             (revised)
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N-PSDB; AAT39041.
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                                                                                                                                                                                                                                                                     L5-MAR-1996;
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04-AUG-1995;
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                                            16-OCT-2003
                                                     22-DEC-1996
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                      AAW04893;
                                                                                                                                                                                           Protein
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A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT3093 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodies can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae; antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria meningitidis antigen, highly conserved between different strains - useful for prodn. of antibodies for immunisation against, diagnosis of, N. meningitidis infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
                                                                                Proteinase K resistant N. meningitidis 22 kD surface protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.0%; Score 825; DB 2; Length 174; 94.3%; Pred. No. 4.8e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rioux C;
                                                                                                                                                                                                                                                                                                                    1. .19
/label= sig_peptide
                                                                                                                                                                                                                                                                                                                                                                 20. .174
/label= mat_protein
                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                           Neisseria meningitidis; strain b2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Martin D, Hamel J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Fig 10; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96WO-CA000157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00406362.
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Best Local Similarity 94.3%;
Matches 164; Conservative
                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BIO VAC INC.
(revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1996-443187/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAT39042
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RESULT 11 ABG91063

RESULT 10 AAW04894

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antibody; detection; probe; surface protein.
                                                                                                                                                                                                                                                WPI; 1996-443187/44.
N-PSDB; AAT39040.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 175 AA;
                                                                                                         WO9629412-A1
                                                                                                                                                   15-MAR-1996;
                                                                                                                                                                                  04-AUG-1995;
                                                                                                                                                                                                                            Brodeur BR,
                                                                                                                                                                       17-MAR-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JUN-2004
                                                                                                                              26-SEP-1996
                       Neisseria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Si
Matches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                          Protein
                                                     Peptide
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ID ADL2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new gram-negative bacterial bleb presenting on its surface the PorB outer membrane protein from Chlamydia trachlomatis, or a protective antigen from C. pneumoniae. The invention is useful for preventing C. trachomatis or C. pneumoniae infection in a host. The present amino acid sequence represents a Neisseria gonorrhoeae protein as described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                         Novel gram-negative bacterial bleb presenting on its surface PorB outer membrane protein from Chlamydia trachomatis or protective antigen from Chlamydia pneumoniae, useful for preventing Chlamydia infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKALAALIAALIALALPAAALAEGASGFYVQADAAHAKASSSIGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKALATLIALPAAALAEGASGFYVOADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteinase K reistant; Neisseria meningitidis; Neisseria gonorrhoeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                  Gram-negative bacterial bleb; PorB; outer membrane protein;
Chlamydia trachomatis infection; Chlamydia pneumoniae infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteinase K resistant N. meningitidis 22 kD surface protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Indels
                                                                                                                                                                                                                                                          Poolman J, Verlant VGCL;
                                                             Neisseria gonorrhoeae outer membrane protein #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 825; DB 5;
Pred. No. 4.8e-82;
2; Mismatches 8
                                                                                                        protective antigen; antibacterial; vaccine.
                                                                                                                                                                                                                                   (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
standard; protein; 174 AA
                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 54; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW04892 standard; protein; 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.0%;
                                                                                                                                                                                           08-FEB-2002; 2002WO-EP001356.
                                                                                                                                                                                                                08-FEB-2001; 2001GB-00003169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                          (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 164; Conservative
                                                                                                                                                                                                                                                          Berthet FJ, Lobet Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (revised)
                                                                                                                             Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                              WPI; 2002-657510/70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                         N-PSDB; ABS67381
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 174 AA;
                                          29-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-OCT-2003
22-DEC-1996
                                                                                                                                                                       15-AUG-2002
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                     ABG91063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW04892;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local (
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ID AAW0
XX
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A proteinase K resistant surface protein has been isolated from 4 strains of N. meningitidis (AAT39039 to AAT39042). The isolated 22 kD antigen, antigenic fragments of antibodises can be used in a vaccine for the prevention of infection by N. meningitidis or by N. gonorrhoeae in humans. The antibodies may also be used diagnostically to detect N. meningitidis infection. The antigen may also be used to detect antibodies specific to N. meningitidis antigen. DNA sequences encoding the antigen, or their fragments, can be used as probes for the detection of pathogenic Neisseria bacteria. (Updated on 16-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKKALAALIALALPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Neisseria meningitidis antigen, highly conserved between different
strains - useful for prodn. of antibodies for immunisation against,
diagnosis of, N. meningitidis infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutein; mutant; NspA; vaccine; antibacterial; meningitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N meningitidis strain 608B modified NspA protein #3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 824.5; DB 2;
Pred. No. 5.5e-82;
0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hamel J, Rioux C;
meningitidis; strain MCH88

    19
    label= sig_peptide

                                                                                                                                                                20. .175 __ /
/label= mat_protein
                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; Fig 8; 117pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          96WO-CA000157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95US-00406362.
95US-0001983P.
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95.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADL24385 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IAFB-) IAF BIO VAC INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Martin D,
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The present invention relates to a pharmaceutical composition comprising. a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608B, where the polypeptide is the NspA protein. The composition is useful for inducing an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection meningitidis, N. gonorrhoeae, N. lactamica and N. polysaccharea. It is useful for treatment or prophylaxis of meningitis and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is a modified version of the Neisseria meningitidis strain 608B NspA protein. Note: This sequence is not shown in the specification but has been created based on the information given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                      Composition comprising liposome associated with isolated polypeptide or polynucleotide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MKKALATLIALALPAALAEGASGFYVQADAAHAK-----KGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                 Key Location/Qualifiers
Misc-difference 35. 36
/note= "wild-type NspA residues 36-43 deleted"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94.5%; Score 820; DB 8; Length 166; 95.4%; Pred. No. 1.6e-81; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and the wild-type NspA protein shown in Figure 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; infection; vaccine; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N. gonorrhoeae amino acid sequence SEQ ID 2512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABP77991 standard; protein; 175 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page; 79pp; English.
                                                                                                                                                                                            29-AUG-2003; 2003WO-CA001452
                                                                                                                                                                                                                              30-AUG-2002; 2002US-0406980P
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                                                                                                                                                                                                                                                                 (SHIR-) SHIRE BIOCHEM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 95.4
Matches 166; Conservative
Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                   WPI; 2004-239123/22
                                                                                                                                                                                                                                                                                                    Rioux S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 166 AA;
                                                                                                                        WO2004019976-A2
                                                                                                                                                                                                                                                                                                                                                                                                                       meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-MAR-2003
                                                                                                                                                                                                                                                                                                    Martin D,
                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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The present invention relates to proteins from Neisseria gonorrhoeae. Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing N. gonorrhoeae infection, this may be in the form of a vaccine or gene therapy. Sequences given in records ABPR1074.36-ABPR1046 represent nucleic acid molecules of the invention

New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection.

Masignani V,

Pizza M,

Fontana MR,

(CHIR-) CHIRON SPA

WPI; 2003-058415/05.

N-PSDB; ABZ38961

12-FEB-2002; 2002WO-IB002069.

Neisseria gonorrhoeae.

WO200279243-A2

10-OCT-2002

Disclosure; Page 371; 815pp; English

119

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61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                                                                                                                                                                                                                             1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                     1 MKKALAALIALAAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                    120 FSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
Misc-difference 151. .152
/note= "wild-type NspA residues 152-163 deleted"
                                                                                                                                                                                                                                                               DB 6; Length 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutein; mutant; NspA; vaccine; antibacterial; meningitis.
                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                               N meningitidis strain 608B modified NspA protein #5
                                                                                                                                                                                                                                                              93.3%; Score 809.5; DB 6 93.1%; Pred. No. 2.5e-80;
                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                  ADL24387 standard; protein; 162 AA
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.1%;
Matches 163; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neisseria meningitidis.
                                                                                                                                                                                                                                               Sequence 175 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-JUN-2004
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Composition comprising liposome associated with isolated polypeptide or polymorlectide derived from Neisseria meningitidis strain 608B, or its fragment or analog, useful for inducing an immune response against N. meningitidis.
                                                                                                                                  Example 4; Page; 79pp; English.
29-AUG-2003; 2003WO-CA001452.
                  30-AUG-2002; 2002US-0406980P.
                                   (SHIR-) SHIRE BIOCHEM INC.
                                                                      WPI; 2004-239123/22.
                                                     Martin D, Rioux S;
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The present invention relates to a pharmaceutical composition comprising a liposome associated with an isolated polypeptide derived from Neisseria meningitidis strain 608B, where the polypeptide is the NPA protein. The composition is useful for inducing an immune response against N. meningitidis, for preventing and/or treating N. meningitidis infection and for treating and/or treating neisserial infection chosen from N. meningitidis, N. gonornhoeae, N. lactamica and N. polysaccharea. It is useful for treatment or prophylaxis of meningitis and meningoccaemia, in a host. The host is a mammal, preferably a human and more preferably an adult human. The present sequence is a modified version of the Neisseria meningitidis strain 608B NspA protein. Note: This sequence is not shown in the specification but has been created based on the information given and the wild-type NspA protein shown in Figure 1.

Sequence 162 AA;

Query Match 91.5%; Score 794; DB 8; Length 162; Best Local Similarity 93.1%; Pred. No. 1.1e-78; Matches 162; Conservative 0; Mismatches 0; Indels 12; Gaps

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61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120 PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120 9 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174 61 121 ద g ò ò

121

Search completed: May 19, 2005, 20:55:00 Job time : 304 Bec8

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149, App 57, App 12284, A 5331, Ap 5, Appli 5146, Ap 30094, Ap 7781, Ap

Sequence Sequence Sequence Sequence Sequence Sequence

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OM protein

Run on:

Sequence:

Searched:

Database

Result

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RESULT 1

US-08-913-362-2

Sequence 2, Application US/08913362

Fatent No. 6287-2

GENERAL INFORMATION:
APPLICANT: Berdeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
APPLICANT: RAIOUX, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE ADDRESS:
ADDRESSES POLEY & Lardner
STREET: 3000 K Street, N.W., Suite 500
CONFUTR: 1000 K Street, N.W., Suite 500
STATE: D.C.
COUNTRY: USA
ZIP: 2000-55109
COMPUTER: EN POLEY WISH
COMPUTER: EN POLEY WISH
COMPUTER: EN PARTICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION NUMBER: US 08/406,362
FILING DATE: 13-NOV-1995
ATTURNER APPLICATION NUMBER: US 08/406,362
FILING DATE: 13-NOV-1995
FILING 
                                                                         US-09-059-584-57
US-09-902-540-12284
US-09-902-540-12284
US-09-322-5331
US-09-322-5331
US-09-322-914-30094
US-09-328-352-781
US-09-418-980-8
US-09-902-540-14682
US-09-902-540-14682
US-09-903-540-14682
US-09-903-540-14682
US-09-903-540-14682
US-09-903-2684-56
US-09-903-2676
                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
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TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (202) 672-5300
(202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein US-08-913-362-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
TOPOLOGY:
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Sequence 2, Appli
Sequence 30, Appli
Sequence 30, Appli
Sequence 4, Appli
Sequence 20, Appli
Sequence 20, Appl
Sequence 24, Appl
Sequence 245, Appl
Sequence 7245, Appli
Sequence 7684, Appli
Sequence 7684, Appli
Sequence 7684, Appli
Sequence 7792, Appli
Sequence 7792, Appli
Sequence 7451, Appli
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Sequence 2, Appli
Sequence 2, Appli
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Sequence 11, Appl
                                                                                                                                      May 19, 2005, 20:41:43; Search time 113 Seconds (without alignments) 114.946 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 15,
                                                                                                                                                                                                                                                                    1 MKKALATLIALALPAAALAE........VNTVKNVRSGELSVGVRVKF 174
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Sequence 7,
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(Ggn2_6/ptodata/1/iaa/5A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/5B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6A_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/6B_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
(Ggn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-913-362-6

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US-08-913-362-8

US-08-913-362-4

US-08-913-362-4

US-08-913-362-4

US-08-913-362-26

US-08-913-362-26

US-09-540-238-236-24

US-09-540-238-7922

US-09-543-681A-7922

US-09-543-681A-7922

US-09-543-681A-7841

US-09-540-236-7922

US-09-164-714-7

US-09-164-714-7

US-09-336-4748-3

US-09-336-4748-3

US-09-952-2678-3

US-08-457-9278-2

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US-08-457-9278-2
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US-09-336-447A-11
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                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                          513545 segs, 74649064 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                                                                                           US-10-650-123-2
868
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Match Length
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838.5
825.5
824.5
135
135
113.5
109.5
93
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DB 3; Length 174;

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61 PAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                  61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF
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                                                                                                                        121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                       APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Martin, Denis
APPLICANT: Marel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 838.5; DB 3; Length 175;
Pred. No. 2.2e-89;
0; Mismatches 4; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR.1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: BERIC, Stephen A:
NAME: BERIC, Stephen A:
REGESTERATION NUMBER: 29,768
REGESTERATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               047998/0128
                                                                                                                                                                                                                                                                                                                                  Sequence 30, Application US/08913362
Patent No. 6287574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30:
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Best Local Similarity 97.1%;
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 175 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 FAVDYTRYKNYKAPSTDFKLYSIGASVIYDFDTQSPVKPYFGARLSLNRASAHLGGSDSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
121 FSQTSXGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174
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0
                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hamel, Josee
APPLICANT: Hamel, Josee
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 825; DB 3; Length 174;
Pred. No. 7.9e-88;
2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: 0.05.0007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 60/001,983
PILING DATE: US-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAMME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 047998/0128
TELECOMMUNICATION INMBER: 047998/0128
                                                                                                                                                                                                                                                                                                                                                                STREET: 3000 K Street, N.W., Suite 500
                                                                                                  Sequence 8, Application US/08913362
Patent No. 6287574
                                                                                                                                                                                                                                                                                                                                            Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 94.3%;
Matches 164; Conservative
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INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (202) 672-5300
(202) 672-5399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-913-362-8
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Sequence 4, Application US/08913362 Patent No. 6287574

US-08-913-362-4

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61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 FAVDYTRYKNYK-APSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Gaps
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APPLICANT: SHARMA, Lawrence Rajendra
TITLE OF INVENTION: ANTIBODIES WHICH BIND MENINGITIS RELATED
TITLE OF INVENTION: HOMOLOGOUS ANTIGENIC SEQUENCES
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3; Length 175;
                 APPLICANT: Hamel, Josee
APPLICANT: Rioux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
TUTNER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/406,362
FILING DATE: 17-MAR-1995
PRIOR APPLICATION NUMBER: US 60/001,983
FILING DATE: 17-MAR-1995
ATTORNEY/AGBWT INFORMATION:
NAME: Bent, Stephen A.

REFERENCE/DOCKET NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
95.0%; Score 824.5; DB 3;
Best Local Similarity 95.4%; Pred. No. 9.1e-88;
Matches 167; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                         STREET: 3000 K Street, N.W., Suite 500 CITY: Washington
                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 2000-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          175 amino acids
  Martin, Denis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                             CITY: Wash
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-127-499A-20
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APPLICANT:
APPLICANT:
APPLICANT:
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unknown
  CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-482-847-20
                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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Patent No. 5556757

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: SHARMA, LAWTENCE Rajendra

APPLICANT: SHARMA, LAWTENCE RAJENTING EPITOPIC SITES FOR

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

TITLE OF INVENTION:

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITT: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
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                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/127,499A
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT: Stephen A.
REGISTRATION NUMBER: 59,768
REFERENCE/DOCKET NUMBER: 51916/102/INBI
TELECOMMUNICATION INFORMATION:
SELEX: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 2007-5109
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,847
FILING DATE: 07-UNN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.6%; Score 135; DB 26.3%; Pred. No. 1.3e tive 20; Mismatches
                   3000 K Street, N.W., Suite 500 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ATLIALALPAALAEGASGFYVQADAAH---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46 FSPRISAGYRINDLRFAVDYTRYKNY---
                                                                                                        ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 26.33
Matches 41; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: unknown
US-08-127-499A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS:
ADDRESSEE:
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US-08-482-847-20
                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
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75 IHPRVSVGYDFGGWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHA 134
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Patent No. 6287574

GENERAL INFORMATION:
APPLICANT: Brodeur, Bernard R
APPLICANT: Martin, Denis
APPLICANT: Hanel, Josee
APPLICANT: Rloux, Clement
TITLE OF INVENTION: PROTEINASE K RESISTANT SURFACE PROTEIN
TITLE OF INVENTION: OF NEISSERIA MENINGITIDIS
NUMBER OF SEQUENCES: 30
CORRESONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER SEADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/913,362
FILING DATE: 13-NOV-1997
RILING DATE: 17-MAR-1995
FILING DATE: 17-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/001,983
FILING DATE: 04-AUG-1995
ATTONEY/AGENT INPOMMATION:
NAME: BERUL, Stephen A:
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80 LYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 15.6%; Score 135; DB 1; Best Local Similarity 26.3%; Pred. No. 1.3e-07; Matches 41; Conservative 20; Mismatches 47
                                                                                                            **REFERENCE/DOCKET NUMBER: 29,768
**REFERENCE/DOCKET NUMBER: 51916/104/INBI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELERA: (202)672-5399
TELERA: 904136
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 170 amino acids
TTRANDEDNIPS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46 FSPRISAGYRINDLRFAVDYTRYKNY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 ATLIALALPAAALAEGASGFYVQADAAH-----
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/127,499
FILING DATE: 28-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
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SABERAL INCOMENTAL GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709-1002-001
CURRENT APPLICATION NUMBER: US/09/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR PELING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7922
LENGTH: 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: GARY BRETON:
APPLICANT: GARY BRETON:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILI
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT APPLICATION NUMBER: US 409/543, 681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
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                          7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98 KPY--LGARL-----SLNRASVDLGGSDSFSQTSIGLGVL--TGVSYAVTPNVDLDAG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     140 DVYTRIGGMVWRADSTATINATSA -- GTQKRFSENDTGVSPVFALGTEYAITPNIATRLE 197
                                                                                                                                                                                                                                         100 YLGARLSLNRASVDLGGSDSFSQTSIGLGV-----LTGVSYAVTPNVDLDAGYRY-NYI 152
                                                                                                                                                     45 -GFSPRISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIY----DFDTOSPVKP 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23 MKK---TAIALAVAVAAFATAAQAAPKDNTWYTGGKLGWSQYQSTGNNWDGVNIGNGSTH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 SPRIS----AGYRIND---LRFAVDYTRYKNYKAPSTD--FKLYSIGASAIYDFDTQSPV 97
                                                                                                          64
                                                                                             43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MKKALATLIALALPAAALAEGASG-----FYVQADAAHAKASS-----SLGSAKGF
                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12.0%; Score 104.5; DB 4; Length 384; 26.1%; Pred. No. 0.0016; live 27; Mismatches 86; Indels 43.
                                                                    1 MKKALATLIA--LALPAALAEGASGFYVQADAAHAKASSSLGSAK--
      25.2%; Pred. No. 0.00014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          147 YRY-NYIGKVNTVKNVR--SGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7922, Application US/09543681A
Patent No. 6605709
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7684, Application US/09543681A Patent No. 6605709
                                                                                                                                                                                                                                                                                                                                                                      166 GKDGNRDNTLADGAYAGVNFRF 187
                                                                                                                                                                                                                                                                                                                           153 GKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                               65 DGDSVGLGMGYNFNLGPF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 26.19
55; Conservative
                        51; Conservative
Best Local Similarity
Matches 51; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-543-681A-7922
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Best Local
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GENERAL INFORMATION:

APPLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT FILING DATE: 2000-04-04

SEQ ID NOS: 3840

LENGTH: 98

LENGTH: 98
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Sequence 13699, Application US/09489039A

Fatent No. 6610836

GENERAL INFORMATION:
APPLICANT: Gary Breton et. al

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 2000-01-27

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 13699
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 98;
                                                                                                                                                                                                                                                                                                                                                  Length 25;
                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                             15.3%; Score 133; DB 3; I 100.0%; Pred. No. 1.3e-08; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 113.5; DB 4
Pred. No. 1.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.6%; Score 109.5;
    047998/0128
                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FAVDYTRYKNYKAPSTDFKLYSIGA 85
                                                                                                                                                                                                              MOLECULE TYPE: protein
ORIGINAL SUNCE:
ORGANISM: Neisseria meningitidis
STRAIN: 608B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2245, Application US/09540236 Patent No. 6673910
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  REFERENCE/DOCKET NUMBER: 04
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5390
TELEFAX: (202) 672-539
                                                                                  TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.1%;
37.9%;
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Best Local Similarity 100.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: M.catarrhalis
US-09-540-236-2245
                                                                                                                                                                           amino acid
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US-09-540-236-2792
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARROGANOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ARROGANOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 TGTWGİRAĞQOFEQGRX---YATYENISDTSSGNKLRQ--QNLLGSYDAFLPIGDNNTKL 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 YLGARLSLNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRY----- 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 N-DLRFAV------DYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGA- 103
                                                                                                                                                                                                                                                                                                                                                                 66 BFDNQWGMIGSFVYTHQGYDY-HWNSRKIGSIDLDYYSLAAGPVYRFNDYISAYGLVGVA 124
                                                                                                                                                                                                                                                                                                                                                                                                                          ----RESLNRASVDLGGSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVK 159
                                                                                                                                                                                                                                                                                   ----ISAGYRINDLRFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTOSPV----KP
                                                                                                                                                                                                                                                      2 KKALATLI--ALALPAA-ALAEGASGFYVQADAAHAKASSS--LGSAKGFSPRISAGYRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 KALATI-IALALPAALAEGASGFYVQADAAHAKASSSLGSAKGF----SPR----
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                                                                                                                                                                 10.7%; Score 93; DB 4; Length 190; 26.0%; Pred. No. 0.012; ive 32; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 PHGGNKLGSLDLHS---SSQFYLGANYKF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----NYIGKVNTVKNVRSGELSVGVRVKF 174
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Patent No. 6551795
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7684
LENGTH: 190
                                                                                                    ; ORGANISM: Proteus mirabilis
US-09-543-681A-7684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 -VGTWMLGLGYR 189
                                                                                                                                                                     Query Match
Best Local Similarity 26.0
Matches 50; Conservative
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Best Local Similarity
Matches 49; Conserv
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US-09-252-991A-19759
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RESULT 14

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Sequence 2792, Application US/09540236

Sequence 2792, Application US/09540236

BENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Gary L. Brecon et al.
APPLICANT: Gary L. Brecon et al.
TITLE OF INVENTION: WOLLEIC ACID AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARFITILE OF INVENTION: POW DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2005-001
CURRENT PELLING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840

FENCH AND 2792
FENCH AND 2792
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Factor No. 6610836

GENERAL INFORMATION:

APPLICANT: GATY Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT FILING DATE: 1999-01-27

NUMBER OF SEQ ID NOS: 14342

SEQ ID NOS: 14342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 GYNF-DQNFGVEABFVGSDAKEFNAGMSPVKGDVKSFGAYGTYRYNFINTPF--YAKGKL 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 SLNRASVDLGG-----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVK 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 RFAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLN-----RASV 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --SDSFSQTSIGLG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKK-ALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDL
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10.3%; Score 89.5; DB 4; Length 385;
Best Local Similarity 24.1%; Pred. No. 0.088;
Matches 55; Conservative 23; Mismatches 69; Indels 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.3%; Score 89.5; DB 26.7%; Pred. No. 0.03; tive 29; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160 NVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 -- DANAISLGTHLAF 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 26.7%
Matches 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            , ORGANISM: M.catarrhalis
US-09-540-236-2792
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OM protein - protein search, using sw model

Run on:

May 19, 2005, 20:34:09; Search time 69 Seconds (without alignments) 242.634 Million cell updates/sec

US-10-650-123-2 868 1 MKKALATLIALALPAAALAE......VNTVKNVRSGELSVGVRVKF 174 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

SUMMARIES	Description	outer membrane pro	outer membrane pro	protein		protein	protein		protein	protein	protein	protein-	protein	opacity protein P.	protein	opacity protein op	protein	protein	protein	protein	protein	protein		protein	protein	protein	protein	protein	protein	;
SUMM	ID	G81174	B81932	816610	S16611	S16613	S16612	KONH0	836343	S16614	S16616	S08514	\$20043	S04380	KONH2C	S72343	836329	S16617	S36342	S36341	836350	KONH8	S36348	836349	S16619	836346	PL0038	363	F64124	2863
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	Length	174	174	261	260	338	258	260	237	257	266	258	254	270	268	283	234	282	234	234	233	234	234	238	261	243	248	238	178	239
d	Query Match	99.5			27.9		27.8	27.8			27.5		-		27.2		26.8		26.7	26.7	56.6	26.0	26.0	26.0			25.5			
	Score	864	854	244.5	242	241.5	241	241	240.5	240.5	239	238	237	237	236.5	236	232.5	232.5	232	232	231	226	226	226	226	224.5	221	219	217	215
	Result No.		7	٣	4	S	9	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		56			

outer membrane protein NMA0862 [imported] - Neisseria meningitidis (strain 22491 serogrou cuter membrane protein NMA0862 [imported] - Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81932
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
A;Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81932
A;Status: preliminary

RESULT 2

opacity protein op	opacity protein op	opacity protein op	opacity protein ho	opacity protein op	opacity protein op	opacity protein-re	opacity protein-re	probable outer mem	outer surface prot	hypothetical prote	probable outer mem	opacity protein op	opacity protein op	heat resistant agg	heat resistant agg
\$28627	S44706	S44707	164187	S77737	S20044	808513	T10256	AH0541	AH3012	G98271	F64066	S16286	S44712	AG3556	I54668
7	~	~	N	~	~	~	N	~	~	~	N	~	~	N	N
247	214	235	121	210	187	168	170	239	281	284	70	201	192	284	264
23.7	23.4	21.8	20.7	17.3	16.2	15.6	15.6	15.2	14.9	14.9	14.6	14.6	14.5	14.1	14.0
205.5	203.5	189.5	180	150.5	141	135	135	132	129.5	129.5	126.5	126.5	126	122	121.5
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

 RESOLDI 1 GBITT4 Guttar membrane nyotein Naza NMBA662 [imported] . Neisseria meningitidis (strain MCS sero	is (strain MC58 serc
 C;Species: Neisseria meningitidis	ום (פרומווו הכסס פביר
 v	T-2004
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E	n, K.E.; Eisen, J.A.
 Hickey, E.K.; Hart, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.	.; Dougnerty, B.A.; .; Pizza, M.
 Science 287, 1809-1815, 2000	
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.K.; Kappuoli, K.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.	.; Kappuoli, K.; ver B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307	
 A,ACCESION: GUII/4	
A Molecule type: DNA	
A;Residues: 1-174 <tet></tet>	
	25876; PIDN:AAF41081
A, Experimental source: serogroup B, strain MC58	
C;Genetics: A;Gene: NWB0663	
Query Match Best Local Similarity 99.4%; Pred. No. 1.4e-69;	
vative 0	Gaps 0;
Qy 1 MKKALATLIALALAPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR	INDLR 60
Db 1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR	INDLR 60
 Qy 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF	GSDSF 120
Db 61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF	GSDSF 120
Qy 121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF 174	174
Db 121 SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVRNVRSGELSAGVRVKF 174	174

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116

82

257 170

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C;Date: 04-Jun-1997 #sequence revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: S16611; S36345; $28624
R;Bhat, K.S.; Gibbs, C.P.; Barrers, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, I Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a famil A;Reference number: S16610; MUID:92114767; PMID:1815562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Experimental source: strain MS11, variant F3
A,Note: expression of opacity proteins is regulated by the number of translated repeat el
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Experimental source: strain M311, variant 4.8
A, Note: the authors did not translate the sequence for the signal peptide
A, Note: expression of opacity proteins is regulated by the number of translated repeat
A, Note: expression of opacity proteins is regulated by the number of translated repeat
B, Note to be start codon in frame with the rest of the protein
B, Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A, Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms A; Reference number: S36328; MUID:93178439; PMID:8440254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      opacity protein opaJ precursor - Neisseria gonorrhoeae (strain MS11) (fragments) N,Alternate names: outer membrane protein opa58
                                                                                                                                                                                                                                                                   141 LGLSAVYDFKLNDKFKPYIGARVAYGHVRHSIDSTKKTTEVTTILHGPGTTPTVYPGKNT 200
                                                                                                                                                                                                                                                                                                                                                                                           201 QNAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENTR-FKTHEASLGV
                                                                                                                   81 SVGYDFGGWRIAADYARYRKWNNNKYSVSIKELLRNKGNGNRTDLKAENQENGTFHAVSS
                                                                                                                                                                                                                                                                                                                                                       117 ----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;MOlecule type: DNA
A;Residues: 24-260 <KUP>
A;Cross-references: EMBL:Z18937; NID:g49333; PIDN:CAA79370.1; PID:g940799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reywords: cell surface component; transmembrane protein 11-10,11-23/Domain: signal sequence (fragments) #status predicted 42-260/Product: opacity protein opaJ #status predicted <MAT> 34-42/Domain: transmembrane #status predicted <TM1> +42/Domain: extracellular #status predicted <TM1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;134-148/Domain: transmembrane #status predicted <TM4>;154-164/Domain: transmembrane #status predicted <TM5>;165-211/Domain: extracellular #status predicted <EXT3>;170-217/Region: hypervariable region HV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      #status predicted <TM7>
#status predicted <EXT4>
#status predicted <TM8>
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F)75-83/Domain: transmembrane #status predicted <TM2>
F)88-94/Domain: transmembrane #status predicted <TM3>
F)95-133/Domain: extracellular #status predicted <EXT2>
F)101-128/Region: hypervariable region HV1
F)134-148/Domain: transmembrane #status predicted <TM4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  #status predicted <TM6>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 242; DB 2;
Pred. No. 3.9e-14;
                                                                                                                                                                                               83 IGASAIYDFDTQSPVKPYLGARLSLN--RASVD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q04882; EMBL:X52371
                                           SAGYRINDLRFAVDYTRYKNY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.9%;
29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;212-224/Domain: transmembrane
F;228-236/Domain: transmembrane
F;237-251/Domain: extracellular
F;252-260/Domain: transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene: opaJ
Superfamily: opacity protein
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-260 < BHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 RYRF 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Accession: S16611
                                           51
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Substitution opak precursor - Neisseria gonorrhoeae (strain MS11) (fragments)

NiAlternate names: outer membrane protein opak

C;Species: Neisseria gonorrhoeae

A;Variety: strain MS11

C;Date: 13-4nn-1995 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997

C;Accession: Si6tio

R;Bhat, K.S; Gibbs, C.P; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch,

Mol. Microbiol. S; 1899-1901, 1991

A;Attle: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami

A;Accession: Si6tio

A;Molecule type: DNA

A;Rosidues: 1.261 - 48Hb.

A;Accession: Si6tio

A;Molecule type: DNA

A;Rosidues: 1.261 - 48Hb.

A;Cross-references: EMBL:X5264

A;Rosidues: 1.261 - 48Hb.

A;Cross-references: EMBL:X52364

A;Rosidues: 1.261 - 48Hb.

A;Ros
                                                                               GB:AL157959; NID:g7379424; PIDN:CAB8414
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                               1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 SQTSTGLGVLAGVSXAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGVRVKF
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                                                                                                                                                                                                                                                                       98.4%; Score 854; DB 2; Length 174; 98.3%; Pred. No. 1.1e-68;
                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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F;155-165/Domain: transmembrane #status predicted <TM5>
F;166-212//Domain: extracellular #status predicted <EXT3>
F;171-218/Region: hypervariable region HV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;213-225/Domain: transmembrane #status predicted <TM6>,
;229-237/Domain: transmembrane #status predicted <TW7>,
;238-252/Domain: extracellular #status predicted <EXTM5,
;253-261/Domain: transmembrane #status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                               3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.2%; Score 244.5; DB 2 29.9%; Pred. No. 2.3e-14; ive 26; Mismatches 58
                               A;Residues: 1-174 <PAR>
A;Cross-references: UNIPROT:P95372; GB:AL162754;
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: nspA; NNA0862
                                                                                                                                                                                                                                                                                                               Pred. No. 1.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;213-225/Domain: transmembrane
                                                                                                                                                                                                                                                                                                           Best Local Similarity 98.3
Matches 171; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 29.9
Matches 73; Conservative
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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repeat

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Matches 76; Conservative 27; Mismatches 67; Indels 88; Gaps 10;	
2 KKALATLIALALPAALAEGASGFYVQADAAHAKASSSLGSAKGFS- 4	157 HPRVSVGYDFGGWRIAADYARYRKWNDNKYSVDIKELENKNONKRDLKTENQENGTFHAV 21
Db 6 KKPSLLPSSLLPSSAAQAAGEDHGRGPYVQADLAYAYEHITHDYPEQTDPSKGKISTVSD 65	OY 81 YSIGASAIYDEDIQSPVKPYLGARLSLNRAS'NDLGG 116 - - - - - - - - - - - - - - - - - - -
Qy 48RAPSIDFK 79	117SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKGVVRSGELSVGVR
Qy 80LYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLG 115	Db 277 TQNAHHQSNSIRRVGLGVIAGVGFDITPKLTLDTGYRYHYWGRLENTR-FKTHEASLGVR 335 Qy 172 VKF 174 :
116 GSDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVN	Db 336 YRF 338
Db 186 GPGTTPTVYPGKNTQDAHRESDSIRRVGLGAVAGVGIDITPNLTLDAGYRYHYWGRLE 243 Qy 157 TVKNVRSGELSVGVRVKF 174	RESULT 6 S16612 opacity protein opaE precursor - Neisseria gonorrhoeae (strain MS11) (fragments) C.Species: Neisseria gonorrhoeae
FF7	C;Date 04-Jun 1937 #Sequence_revision 17-Oct-1997 #text_change 17-Oct-1997 #Sequence_revision 17-Oct-1997 #Sequence_revision 17-Oct-1997 #Sequence_revision 17-Oct-1997 #Sequence_revision 17-Oct-1997 #Sequence_revision 17-Oct-1997 #Sequence 18-Oct-1997 #Sequence 18
S16613 opacity protein opaB precursor - Neisseria gonorrhoeae (strain MS11) (fragments) C;Species: Neisseria gonorrhoeae	889-1901, 1991 proteins of Neisseria gonorr S16610; MUID:92114767; PMID:1
A,Variety: strain MS11 C;Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997	A, Accession: S16612 A; McCecule type: DNA A; Molecule type: DNA A Description: 1-258 APHA
Cynccession: Sights, S.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Migrobiol. 5, 1889-1901, 1991	A,resignes: 1.250 Juny. A;crosw.references: EMBLX52369 A;Experimental source: strain MS11, variant 4.8
A.fitle: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami A.Reference number: S16610; MUID:92114767; PMID:1815562	A; Note: the authors did not translate the sequence for the signal peptide A; Note: expression of opacity proteins is regulated by the number of translated repeat electrons as the start codon in frame with the rest of the protein
A;Molecule type: DWA A;Residues: 1-338 <bha></bha>	C;Genetics: A;Gene: opaE
A.Crose-references: EMBL:X52373 A.Experimental source: Strain MS11, variant 4.8 A.Note: the authors did not translate the secuence for the signal peptide	C.Superfamily: opacity protein C.Keywords: cell surface component; transmembrane protein F:1-10.11-23/Domain: signal sequence (fragments) #status predicted <sig></sig>
A,Note: expression of opacity proteins is regulated by the number of translated repeat e of repeats place the start codon in frame with the rest of the protein	F;24-258/Product: opacity protein opaE #status predicted <mat> F;34-42/Domain: transmembrane #status predicted <tml> F:34-42/Domain: transmembrane #status predicted <tml> F:43-74/Domain: extracellular #status oredicted <tml></tml></tml></tml></mat>
Vyenetrob. AyGener opposity protein	F:50-60/Region: semivariants recommended for the F:55-60/Region: semivariants for the F:75-83/Domain: transmembirane #status predicted <tm2></tm2>
C, Keywords: cell surface component; transmembrane protein F;1-13,14-104/Domain: signal sequence (fragments) #status predicted <sig></sig>	F:88-94/Domain: transmembrane #status predicted <tm3> F:95-131/Domain: extracellular #status predicted <ext2></ext2></tm3>
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Fil24-155/Domain: extracellular #Status predicted <6xii>Fil24-155/Region: semivariable region Fil32-141/Region: semivariable region Fil6-164/Domain: transmembrane #tratus predicted <7M2>	Filoz-10/Jomann: Transmembrane #status predicted <1m3> Filo3-209/Domain: extracellular #status predicted <8XT3> Fil68-215/Region: byoervariable region HV2
7:169-175/Domain: transmembrane #status predicted <tm3> F:169-175/Domain: extracellular #status predicted <ext2></ext2></tm3>	transmembrane #status
F;182-207/Region: hypervariable region HV1 F;213-227/Domain: transmembrane #status predicted <tm4></tm4>	extracellular #status predicted transmembrane #status predicted
r;224-269/Domain: extractinian #statub predicted <ea13> F;233-243/Domain: transmembrane #status predicted <tms> F;249-295/Region: hypervariable region HV2 F;290-302/Domain: transmembrane #status predicted <tm6></tm6></tms></ea13>	Query Match 27.8%; Score 241; DB 2; Length 258; Best Local Similarity 29.7%; Pred. No. 4.7e-14; Matches 76; Conservative 26; Mismatches 68; Indels 86; Gaps 10;
306-314/Domain: transmembrane #status 315-329/Domain: extracellular #status 330-338/Domain: transmembrane #status	2 KKALATLIALALPAAAL! : :
Match 27.8%; Score	6 KKPSLLFSSLLFSSAQAAGEDHGRGPYVQADLAYAYEHITHDYPEPTGTKKDKISTVSD 6
21	OY 45GFSPKILSAGYKINDLKKAVDYIKYK-NYKARSIDEK79
Qy 10 ALALPAALAEG-ASGEYVQADAAHAKASSSLGSAKGF 46	Qy 80LYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGG- 116 -
47 SPRISAGYRIDLRFAVDYTRYKNYKAPSTDFK	DFKLNDKFKPY1GAR

6

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C;Accession: S36343; S26626 —
R;Kupsch, E.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
EMBO J. 12, 641-650, 1993
A;Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms dis A;Reference number: S36328; MUID:93178439; PMID:8440254
A;Accession: S36343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIDROT:Q04880; EMBL:Z18935; NID:g49331; PIDN:CAA79368.1; PID:g940797; A;Experimental source: strain MS11, variant F3
A;Note: expression of opacity proteins is regulated by the number of translated repeat el of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 -----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 74 HSIHPRVSVGYDFGGWRIAADYARYRKWSDNKYSVSIKNMRVHKHNSNRKNLKTENQENG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ------KNYKAPSTD-- 77
                                                                                                                                                                                                                                                                                                                                                                                                 14 SSLLFSSAAQAASEDGGRGPYVQADLAYAYEHITHDYPKPTDPSKGKISTVSDYFRNIRT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C.Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C.Accession: S36343; S28626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --FKLYSIGASAIYDFDTQSPVKPYLGARLSLN--RASVD-------LGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                          84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
                                                                                                                                                                                                                                                                                                                          6 ATLIALALPAALAEGASGFYVQADAAHA-----KASSSLGSAKGFS-
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                                                                                                                                                               Length 260;
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;Keywords: cell surface component; transmembrane protein
;1-237/Product: opacity protein opa57 #status predicted <MAT>
;11-19/Domain: transmembrane #status predicted <TM1>
;20-51/Domain: extracellular #status predicted <EXT1>
                                                                                                                                                                                                                                               64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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F;52-60/Domain: transmembrane #status predicted <TW2>
F;52-10/Domain: transmembrane #status predicted <TW3>
F;72-110/Domain: extracellular #status predicted <EXT2>
F;78-105/Region: hypervariable region HV1
F;111-125/Domain: transmembrane #status predicted <TW4>
F;111-126/Domain: transmembrane #status predicted <TW5>
F;147-198/Domain: extracellular #status predicted <TW5>
F;147-198/Region: hypervariable region HV2
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F;228-236/Domain: transmembrane #status predicted <TM7>
F;237-251/Domain: extracellular #status predicted <EXT4>
F;252-260/Domain: transmembrane #status predicted <TM8>
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29.6%; Pred. No. 4.7e-14;
ive 26; Mismatches 58;
                                                                                                                                                           27.8%; Score 241; DB 1;
28.8%; Pred. No. 4.7e-14;
ive 30; Mismatches 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48 ----PRISAGYRINDLRFAVDYTRY----
                                                                                                                             Conservative
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251 EASLGVRYRF 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 71; Conserv
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A; Residues: 1-237 < KUP>
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F;189-201/Domain:
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A Note: the authors translated the codon CCA for residue 32 as Thr
A Note: the authors did not translate the sequence for the signal peptide
A Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
Cell 47, 61-71, 1986
A TILLE: Opacity genes in Neisseria gonorrhoeae: control of phase and antigenic variatic
A Reference number: A90887; MUID:87002493; PMID:3093085
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R;Kupsch, B.M.; Knepper, B.; Kuroki, T.; Heuer, I.; Meyer, T.F.
BMBO J. 12, 641-650, 1993
A;Title: Variable opacity (Opa) outer membrane proteins account for the cell tropisms di
A;Reference number: S36328; MUID:93178439; PMID:8440254
                                                                                                                                                                                                                                                                                                                                                                                                                                           Opacity protein opaC precursor - Neisseria gonorrhoeae (strain MS11) (fragments)
N;Alternate names: opacity protein V0; triosephosphate dehydrogenase
C;Species strain MS11
C;Date: 31.Mar-1899 #sequence revision 17-Oct-1897 #text_change 09-Jul-2004
C;Date: 31.Mar-1899 #sequence revision 17-Oct-1897 #text_change 09-Jul-2004
C;Accession: S16618; A24429; S36228; S28621
R;Bhat, K.S.; Gibbs, C.P.; Barrera, O.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Kupsch, Mol. Microbiol. 5, 1889-1901, 1991
A;Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded by a fami A;Reference number: S16610; MUID:92114767; PMID:1815562
A;Accession: S16610; MUID:92114767; PMID:1815562
A;Accession: Coloure type: DNA
A;Residues: 1-260 cBHA>
A;Accession: Citering MC11286; EMBL:X52370
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A, Molecule type: DNA
A, Residues: 25-260 <STE>
A, Note: this protein is synthesized as a precursor; however, the authors are uncertain
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Riffleyer, T.F.
Riffleyer, DNA
Riffleyer,
        ----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTV 158
                                                      186 GTTPTVYPGKNTQDAHRESDSIRR--VGLGAVAGVGIDITPNLTLDAGYRYHYWGRLENT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 25-260 «KUP>
A;Cross-references: EMBL:Z18927; NID:g49323; PIDN:CAA79360.1; PID:g940789
R;Meyer, T.F.
                                                                                                                                                                       159 KNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                     : :: | |:||| :|
244 R-FKTHEASLGVRYRF 258
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A; Status: preliminary
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Db 126 NQENGTFHAVSSLGLSAVYDFKLNDKFKRPIGARVAYGHVRHSIDSTKKTTKFLTSSYGG 185 Qy 117SDSFSQTSIGLGVLTGVSYAVTBNVDLDAGYRKNYIGKVNTVKNV 161 Db 186 LNPTVYTEENTQNAHHQSNSIRRVGLGVLTGVSPDITPKLTLDTGYRYHYWGRLENTR-F 244 Qy 162 RSGELSVGVRVKF 174 ::	СЪ, fami	C; Suppertantly: opacatry protein C; Suppertantly: opacatry protein C; Suppertantly: opacatry protein paperate predicted csIG> F;1-10,11-23/Domain: signal sequence (fragments) #status predicted cMT> F;24-266/Product: opacity protein opaD #status predicted cMT> F;34-42/Domain: transmembrane #status predicted cTM1> F;33-74/Domain: extracellular #status predicted cTM1> F;51-60/Region: semivariable region F;53-60/Region: semivariable region F;36-33/Domain: transmembrane #status predicted cTM2> F;88-94/Domain: transmembrane #status predicted cTM4> F;101-134/Region: hypervariable region HV2 F;101-134/Region: hypervariable region HV2 F;101-134/Domain: transmembrane #status predicted cTM5> F;101-134/Domain: transmembrane #status predicted cTM5> F;102-217/Domain: transmembrane #status predicted cTM7> F;104-154/Domain: transmembrane #status predicted cTM7> F;234-224/Domain: transmembrane #status predicted cTM7> F;234-224/Domain: transmembrane #status predicted cTM7> F;243-254/Domain: transmembrane #status predicted cTM8> F;258-266/Domain: transmembrane #status predicted cTM8>	Query Match 27.5%; Score 239; DB 2; Length 266; Best Local Similarity 29.0%; Pred. No. 7.3e-14; Matches 76; Conservative 26; Mismatches 70; Indels 90; Gaps 8; Qy 2 KKALATLIALPAAALAEGASGFYVQADAAHA	Db 66 Oy 70 Db 126 Oy 108 Db 186
Qy 17 ALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGY 54 Db 1 ASEDGGRGPYVQADLAYAYEHITHDYPEPTAPNKNKISTVSDYFRNIRTRSVHPRVSVGY 60 Qy 55 RINDLRPAVDYTRYKNY	RESULT 9 S16614 Opacity protein opaF precursor - Neisseria gonorrhoeae (strain MS11) (fragments C, Species: Neisseria gonorrhoeae A, Variety: strain MS11 C; Date: 04-Jun-1997 #sequence_revision 17-Oct-1997 #text_change 17-Oct-1997 C; Accession: S16614 R) Barrera, 0.; Morrison, S.G.; Jaehnig, F.; Stern, A.; Mol. Microbiol. 5, 1889-1901, 1991 A, Title: The opacity proteins of Neisseria gonorrhoeae strain MS11 are encoded A; Reference number: S16610; MUID:92114767; PMID:1815562 A, Accession: S16614 A, Rederidues: L257 cBHA> A, Residues: L257 cBHA> A, Residues: EMBL:XS2368	Albote: the authors translated the sequence for the signal peptide Albote: the authors translated the sequence for the signal peptide Albote: the authors did not translate the sequence for the signal peptide Albote: expression of opacity proteins is regulated by the number of translated repe Albote: expression of opacity proteins is regulated by the number of translated repe Cignetics: Albote: opacity protein Cignetics: Cignetics: Cignetics: Cignetics: Cignetics: Albote: opacity protein Cignetics: Cig	Filb2-lox/Domain: extracellular #Status predicted <tm3> Fil63-208/Domain: extracellular #Status predicted <ext3> Fil68-214/Region: hypervariable region HV2 Fi209-221/Domain: transmembrane #status predicted <tm7> Fi209-233/Domain: transmembrane #status predicted <tm7> Fi234-248/Domain: extracellular #status predicted <ext4> Fi249-257/Domain: transmembrane #status predicted <ext4> Guery Match 27.7%; Score 240.5; DB 2; Length 257; Best Local Similarity 29.2%; Pred. No. 5.2e-14;</ext4></ext4></tm7></tm7></ext3></tm3>	74; Conservative 2. 2 KKALATLIALALPAALAE

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A;Molecule type: DNA
A;Residues: 1.254 cAHO.
A;Residues: 1.254 cAHO.
A;Cross-references: UNIPROT:033388; EWBL:X63108
A;Experimental source: strain FAM18; clone pFLOB1700
A;Note: the nuclectide sequence was submitted to the EMBL Data Library, November 1991
A;Note: unly a part of the translation is shown
A;Note: expression of opacity proteins is regulated by the number of translated repeat el
of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                           C;Accession: S20043
R;Aho, E.L.; Dempsey, J.A.; Hobbs, M.M.; Klapper, D.G.; Cannon, J.G.
Mol. Microbiol. 5, 1429-1437, 1991
A;Telle: Characterization of the opa (class 5) gene family of Neisseria meningitidis.
A;Reference number: S16286; MUID:92157869; PMID:1787795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 SIGASAIYDFDTQSPVKPYLGARLSLN--RASVDL------GGSD----- 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 PRVSVGYDFGDWRIAADYASYRKWNNNKYSVNTKELENKHNNKKDLKTENQENGTFHAAS 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C.Species: Neisseria meningitidis
A.Variety: strain FAM18
C.Date: 04-Jun-1997 #sequence_revision 04-Jun-1997 #text_change 09-Jul-2004
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C. Superfamily: opacity protein
C. Superfamily: opacity protein
C. Superfamily: opacity protein
C. Superfamily: opacity protein
F. 1-19/Domain: signal sequence (fragment) #status predicted <SIG>F. 1-254/Product: opacity protein opaB #status predicted <MAT>F. 31-39/Domain: transmembrane #status predicted <TM1>F. 40-69/Domain: extracellular #status predicted <EXTI>F. 40-59/Domain: transmembrane #status predicted <TM2>F. 70-78/Domain: transmembrane #status predicted <TM2>F. 90-126/Domain: extracellular #status predicted <TM3>F. 90-126/Domain: extracellular #status predicted <EXT2>F. 90-126/Domain: extracellular #status 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27.3%; Score 237; DB 2; Length 254; 28.3%; Pred. No. 1e-13; ive 31; Mismatches 66; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;127-141/Domain: transmembrane #status predicted <TM4>F;147-157/Domain: transmembrane #status predicted <TM5>F;158-205/Domain: extracellular #status predicted <EXT3>F;163-211/Region: hypervariable region HV2
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N,Alternate names: outer membrane protein class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          48 PRISAGYRINDLRFAVDYTRYKNY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 27.3;
Best Local Similarity 28.3;
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               171 RVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RYHF 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: S20043
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R;Stern, A.; Meyer, T.F.
Mol. Microbiol. 1, 5-12, 1987
A;Title: Common mechanism controlling phase and antigenic variation in pathogenic neisse A;Title: Common mechanism controlling phase and antigenic variation in pathogenic neisse A;Title: Common mechanism controlling phase and antigenic variation in pathogenic neisse A;Reference number: S08513, MUID:88260884; PMID:2455211
A;Accession: S08514
A;Molecule type: DNA
A;Residues: 1-258 <STE>
A;Cross-references: UNIPROT: P10170; EMBL:X06445; NID:944906; PID:91333787
A;Experimental source: strain C1938
A;Note: expression of opacity proteins is regulated by the number of translated repeat effected the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <del>U</del>
                                                                                                                                                                                                                                                                   opacity protein-related protein OPM1 precursor - Neisseria meningitidis (strain C1938)
Nalternate names: outer membrane protein class 5
C; Species: Neisseria meningitidis
A; Variety: strain C1938
C; Date: 19-Mar-1997 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C; Accession: 808514
R; Stern, A.; Meyer, T.F.
Mol. Microbiol. 1, 5-12, 1987
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820043
opacity protein B precursor (clone pFLOB1700) - Neisseria meningitidis (strain FAM18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A Gene: opr1

C, Superfamily: opacity protein

C, Superfamily: opacity protein

C, Superfamily: opacity protein

C, Superfamily: opacity protein

E, 1-13, 14-21/Domain: signal sequence (fragments) #status predicted <SIG>
F, 12-258 | Product: opacity protein-related protein OPM1 #status predicted <MAT>
F, 32-358 | Product: opacity protein-related protein OPM1 |
F, 42-73/Domain: transmembrane #status predicted <EXI1>
F, 50-59/Region: semivariable region
F, 74-82/Domain: transmembrane #status predicted <TM2>
F, 87-93/Domain: transmembrane #status predicted <TM3>
F, 87-93/Domain: transmembrane #status predicted <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134 SSLGLSAIYDFKLNDKFKPYIGARVAYGHVKHOVHSVETKTTTVTSKPKGGTPAGGPVIK 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 -----DSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSV 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       194 TDPSKPPYHESHSISSLGLGVIAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEASL 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      74 IHPRVSVGYDFGGWRIAADYASYRKWKESNFSTKKVTEEIKDNYKETKTEHQGNGSFHAT 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KASSSLGS-----AKG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46 FSPRISAGYRINDLRFAVDYTRYK-----L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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F;100-124/Region: hypervariable region HV1
F;130-144/Domain: transmembrane #status predicted <TM4>
F;150-160/Domain: transmembrane #status predicted <TM5>
F;161-209/Domain: extracellular #status predicted <EXT3>
F;166-215/Region: hypervariable region HV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;210-222/Domain: transmembrane #status predicted <TM6>F;226-234/Domain: transmembrane #status predicted <TM7>F;235-249/Domain: extracellular #status predicted <EXT4>F;250-258/Domain: transmembrane #status predicted <TM8>
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Pred. No. 8.7e-14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28.5%; Pred. ....
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                    |:: :: | |:||| :|
GRLENTR-FKTHEASLGVRYRF 266
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Best Local Simil
Matches 70; C
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opacity protein P.II precursor - Neisseria gonorrhoeae (strain F62-SF and others) (fragme C;Species: Neisseria gonorrhoeae
A;Variety: strain F62-SF
A;Variety: strain F62-SF
C;Date: 3.0-Jun-1991 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: S04380; S16504
R;Palmer, L.; Brooks, G.F.; Falkow, S.
192 STQNAYHESHSIRRLGLGVVAGVGFDITPKLTLDTGYRYHNWGRLENTR-FKTHEVSLGM 250
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NiAlternate names: outer membrane protein P.IIc
C;Species: Neisseria gonorrhoeae
A;Variety: strain JG3
A;Variety: strain JG3
C;Date: 31-Mar-1992 #sequence_revision 17-Oct-1997 #text_change 09-Jul-2004
C;Accession: S03095; S16360
R;Van der Ley, P. Mol. Microbiol. 2, 797-806, 1988
Mol. Microbiol. 2, 797-806, 1988
A;Title: Three copies of a single protein II-encoding sequence in the genome of Neisseriate A;Reference number: S03095; MuID:89096501; PMID:3145386
                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-268 < VAN>
A; Cross-references: UNIPROT: P09888; EMBL:X12625
A; Cross-references: UNIPROT: P09888; EMBL:X12625
A; Experimental source: strain JS3
A; Note: 241-Val was also found
A; Note: 241-Val was also found
A; Note: Expression of opacity proteins is regulated by the number of translated repeatel
A; Note: Cross-reference the start codon in frame with the rest of the protein
R; Barrit, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.
Infect. Immun. S5, 2026-2011, 1987
A; Fitle: Antigenic and structural differences among six proteins II expressed by a single
A; Reference number: S16360; MUID:97306843; PMID:3114142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73 HSVHPRVSVGYDFGSWRIAADYARYRKWNNNKYSVSIKELLRNDNSASGVRGHLNIQTQK 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           133 TEHQENGTFHAVSSLGLSTIYDFDTGSRFKPYIGMRVAYGHVRHQVRSVEQETEIITTYP 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115 ---GGSDSFSQ-----TSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 SNGGGKVSLSSKMPPKSAHHQSNSIRRVGLGVIAGVGFDITPNLTLDTGYRYHNWGRLEN 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76 TDFK-----LYSIGASALYDFDTQSPVKPYLGARLSLNRA----SVDL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Keywords: cell surface component; transmembrane protein F;1-10,1-23/Domain: signal sequence (fragments) #status predict F;1-10,1-23/Domain: signal sequence (fragments) #status predict F;1-10,1-23/Domain: ransmembrane #status predicted <TM1>F;34-42/Domain: transmembrane #status predicted <TM1>F;351-60/Region: semivariable region F;75-83/Domain: transmembrane #status predicted <TM2>F;86-94/Domain: transmembrane #status predicted <TM3>F;95-140/Domain: extracellular #status predicted <TM3>F;101-135/Region: hypervariable region HV1
F;11-155/Domain: transmembrane #status predicted <TM3>F;101-135/Region: hypervariable region HV1
F;11-155/Domain: transmembrane #status predicted <TM5>F;101-135/Region: hypervariable region HV2
F;177-225/Region: hypervariable region HV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 ATLIALALPAAALAEGASGFYVQADAAHAKA----SSSLGSAK---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;220-232/Domain: transmembrane #status predicted <TM6>,236-244/Domain: transmembrane #status predicted <TM7>,345-259/Domain: extracellular #status predicted <EXT4>,260-268/Domain: transmembrane #status predicted <TM84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45 -GFSPRISAGYRINDLRFAVDYTRYK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 VKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.2%;
26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: opacity protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: $16360
A; Status: preliminary
A; Molecule type: protein
A; Residues: 24-34 <BAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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Best Local S
Matches 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                    Title: Expression of gonococcal protein II in Escherichia coli by translational fusion
Reference number: S04380; MUID:89343653; PMID:2503682
                                                                                                                                                                                                                                                   A)Cross-references: UNIPROT:050959; EMBL:X15780
A)Experimental source: strain F62-SF, serogroup IB-3; clone F62-SFG1
A;Note: the authors did not translate the sequence of the signal peptide
A;Note: expression of opacity proteins is regulated by the number of translated repeat
of repeats place the start codon in frame with the rest of the protein
K;Taha, M.K.; So, M.; Seifert, H.S.; Billyard, B.; Marchal, C.
BMGO J., 4367-4378, 1988
A;Title: Pilin expression in Neisseria gonorrhoeae is under both positive and negative
A;Reference number: S02017; MUID:89210824; PMID:2854063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: translation not shown
A;Molecule type: DNA
A;Rosidues: 259-270 < 4TAH>
A;Cross-references: EMBL:X13965
A;Cross-references: EMBL:X13965
A;Experimental source: strain MS11A
A;Note: expression of opacity proteins is regulated by the number of translated repeat of repeats place the start codon in frame with the rest of the protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 HLNIQTQKTEHQENGTFHAASSLGLSTIYDFDTGSRFKPYIGARVAYGHVRHQVRSVEQE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYFRNIRTHSVHPRVSVGYDFGGWRIAADYARYRKWNNNKYSVSIKELGRNDNSASGVRG 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AKASSSLGSAK 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: opacity protein
C; Superfamily: opacity protein
C; Superfamily: cell surface component; transmembrane protein
C; Newvords: cell surface component; transmembrane protein
F; 1-10,11-23/Domain: signal sequence (fragments) #status predicted <NAT>
F; 24-270/Product: opacity protein opaK #status predicted <MAT>
F; 34-270/Domain: transmembrane #status predicted <TM1>
F; 34-270/Domain: extracellular #status predicted <TM2>
F; 51-61/Region: semivariable region
F; 76-84/Domain: transmembrane #status predicted <TM3>
F; 96-141/Domain: extracellular #status predicted <TM3>
F; 96-141/Domain: extracellular #status predicted <TM4>
F; 102-136/Region: hypervariable region HV1
F; 142-156/Domain: transmembrane #status predicted <TM5>
F; 162-172/Domain: transmembrane #status predicted <TM5>
F; 173-221/Domain: extracellular #status predicted <TM5>
F; 173-221/Domain: extracellular #status predicted <EXT3>
F; 173-221/Domain: extracellular #status                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NRASVDLGGS-----DSFSQTSIGLGVLTGVSYAVTPNVDLDAGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKPSLLFSSLLFSSAAQAAGEGNGRGPYVQADLAYAYEHITHDYPKPTGAKKGTTISTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --NYKAPSTDFK-----LYSIGASAIYDFDTQSPVKPYLGARLSL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 237; DB 2; Length 270;
Pred. No. 1.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45 GF-----SPRISAGYRINDLRFAVDYTRYK-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;222-234/Domain: transmembrane #status predicted <TM6>
F;238-246/Domain: transmembrane #status predicted <TM7>
F;247-261/Domain: extracellular #status predicted <EXT4>
F;262-270/Domain: transmembrane #status predicted <TM8>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 KKALATLIALALPAALAEG---ASGFYVQADAAH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YNYIGKVNTVKNVRSGELSVGVRVKF 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;178-227/Region: hypervariable region HV2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |: |: : : | |: | XHNWGRLENTR-FKTHEASLGVRYRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27.3%;
27.1%;
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Matches 72: Conserv
                                                                                                                                                                              A;Molecule type: DNA
A;Residues: 1-270 <PAL>
                                                                                                                                      A; Molecule type: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: S16504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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Gaps

89;

67; Indels

; Score 236.5; DB 1; Pred. No. 1.2e-13; 32; Mismatches 67

DB 1; Length 268;

72 75

RESULT 15

opacity protein P.IIc precursor - Neisseria gonorrhoeae (strain JS3) (fragments)

us-10-650-123-2.rpr

```
opacity protein opaH precursor - Neisseria gonorrhoeae (isolate 15063G)
NyAlternate names: cell invasion protein opaH
C;Species: Neisseria gonorrhoeae
A;Variety: isolate 15063G
C;Date: 14-Peb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S72343
R;Waldbeser. L.S.; Ajioka, R.S.; Merz, A.J.; Puaoi, D.; Lin, L.; Thomas, M.; So, M.
Mol. Microbiol. 13, 919-928, 1994
A;Title: The opaH locus of Neisseria gonorrhoeae MS11A is involved in epithelial cell in A;Reference number: S72343; MUID:95115561; PMID:7815949
A;Accession: S72343
A;Accession: S72343
A;Accession: S72343.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-283 *WALD.
A; Cross-references: UNIPROT: Q50943; EMBL: U13708; NID: 9535357; PIDN: AAA74082.1; PID: 95353
A; Residues: 1-283 *WALD.
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A; Note: expression of opacity proteins is regulated by the number of translated repeat cf. Superfamily: opacity protein
C; Superfamily: opacity protein
F; Reywords: cell surface component; transmembrane protein
F; Reywords: cell surface component; transmembrane #status predicted *MAT>
F; Rey-Gomain: transmembrane #status predicted *EMID>
F; Rey-Gomain: extracellular #status predicted *EMID>
F; Reywords: cell universalable region
F; Reywords: cell variable region
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F;95-84/Region: semivariable region
F;99-107/Domain: transmembrane #status predicted <TM2>
F;112-118/Domain: transmembrane #status predicted <TM3>
F;119-155/Domain: extracellular #status predicted <EXT2>
F;125-150/Region: hypervariable region HV1
F;156-170/Domain: transmembrane #status predicted <TM4>
F;176-186/Domain: transmembrane #status predicted <TM5>
F;180-234/Domain: transmembrane #status predicted <TM5>
F;192-240/Region: hypervariable region HV2
F;252-247/Domain: transmembrane #status predicted <TM6>
F;251-259/Domain: extracellular #status predicted <TM6>
F;260-274/Domain: extracellular #status predicted <TM6>
F;260-274/Domain: extracellular #status predicted <TM7>
F;260-274/Domain: transmembrane #status predicted <TM7>
F;275-283/Domain: transmembrane #status predicted <TM8>
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Matches 68; Conservative
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280 RYRF 283
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MEDLINE=99386904; PubMed=1045695B;
Gadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
"Bactericidal and cross-protective activities of a monoclonal antibody directed against Neisseria meningitidis NspA outer membrane protein.";
Infect. Immun. 67:4955-4959(1999).
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SEQUENCE FROM N.A.

STRAIN=M986, NG6/88, and NGP165;

STRAIN=M986, NG6/88, and NGP165;

Moe Gr., Tan S., Granoff D.M.;

I "Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";

L Infect. Immun. 0:0-0(1999).

EMBL; U52066; AAC30001:1 -.

R EMBL; AF175680; AAD53283.1; -.

R EMBL; AF175680; AAD53286.1; -.

R EMBL; AF175680; AAD53286.1; -.

R EMBL; AF175689; AAD53286.1; -.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:0016209; C:membrane; IEA.

R GO; GO:0012094; Poorin activity; IEA.

R Pfam; PF02462; Opacity; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97258610; PubMed=9104804;
Martin D., Cadleux N., Hamel J., Brodeur B.R.;
Highly conserved Neisseria meningitidis surface protein confers
protection against experimental infection.";
J. Bxp. Med. 185:1173-1183 (1997).
                            Q9rqv4
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O079274
Q51013
Q51303
Q9k4t5
Q9k4t5
Q9k753
Q9x9a8
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Neisseriaceae; Neisseria.
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05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Outer membrane protein precursor (Surface protein A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-99270944; PubMed=10338491; Plante M., Cadieux N., Rioux C.R., Hamel J., "Antigenic and molecular conservation of the
                                                                                                                                                                                                                                                                                                       174 AA
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                                                                                                                                                                                          1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                    Length 174;
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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                      E8B02767DDC6FE19 CRC64;
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Last annotation update)
                                                                  100.0%; Score 868; DB 2; 100.0%; Pred. No. 1.5e-69;
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99.5%; Score 864; DB 2;
Best Local Similarity 99.4%; Pred. No. 3.3e-69;
Matches 173; Conservative 0; Mismatches 1;
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                                                                                                                   0; Mismatches
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TIGR; NMB0663; -.
GO; GO:0016200; C:membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
INTERPYO; IPR003394; Porin opacity.
Pfam; PF02462; Opacity; 1.
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                      174 AA; 18425 MW;
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Outer membrane protein NsgA.
OrderedLocusNames=NMB0663;
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                                                                                                                Matches 174; Conservative
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                                                                                             Best Local Similarity
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SEQUENCE 174 AA;
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SIGNAL
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61 FAVDYTRYKNYKAPSTDFKL/YSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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                                                                                                                                                                                                                                                                                                                           STRAIN=CU385;
SOURD STRAIN=CU385;
MOG G.R., Tan S., Granoff D.M.;
"Differences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";
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STRAIN=M136, and BZ232;
Moe G.R., Tan S., Granoff D.M.;
Molfferences in Surface Expression of Neisserial Surface Protein among Neisseria meningitidis Group B strains.";
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                                                                                                                                                                                       Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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EMBL; AF175678; AAD53281.1; -.

EMBL; AF175678; AAD53281.1; -.

EMBL; AF175678; AAD53281.1; -.

EMBL; AF175678; AAD53281.1; -.

EDB; 1P47; X-ray; A=20-174.

GO; GO:0015288; F:porin activity; IEA.

InterPro; IPR033394; Porin opacity.

EMBUS SEQUENCE 174 AA; 18337 MW; E8B02767DDC6E109 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                              Last sequence update)
Last annotation update)
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Pred. No. 3.3e-69;
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EMBL; AF175679; AAD53282.1; -.

EMBL; AF175677; AAD53280.1; -.

HSSP; OSPR177; 1P4T.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0015288; F:porin activity; IEA.
                                                       Created)
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                    Q9RP17;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-UJM-2003 (TrEMBLrel. 24,
Surface protein A.
                                                                                                                                                                                                                                         Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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Best Local Similarity 99.4
Matches 173; Conservative
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SEQUENCE
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MEDLINE=99386904; PubMed=10456958;
MEDLINE=99386904; Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
"Bactericidal and cross-protective activities of a monoclonal antibody
directed against Neisseria meningitidis NspA outer membrane protein.";
Infect. Immun. 67:4955-4959(1999).
EMBL, US2068; AAB41580.1; -.
PIR; B81932; B81932.
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1-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAY-2003 (TrEMBLrel. 24, Last annotation update)
01-UNN-2003 (FREMBLrel. 24, Last annotation update)
01-UNN-2003 (FREMBLrel. 24, Last annotation update)
01-State membrane protein precursor.
Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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                                                         Length 174;
InterPro; IPR003394; Porin_opacity.
Pfam; PF02462; Opacity; 1.
SEQUENCE 174 AA; 18385 MW; ECF6F39A9286910E CRC64;
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                                                     Score 857; DB 2;
Pred. No. 1.4e-68;
1; Mismatches 2
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GO; GO:0016020; C:membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
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                                                      98.7%;
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Signal.
                                                     Query Match
Best Local Similarity 98.33
Matches 171; Conservative
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PRELIMINARY;

Q7AR60 Q7AR60;

RESULT 6 Q7AR60 ID Q7A AC Q7A

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61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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STRAIN=22491 / Serogroup A / Serotype 4A;
MEDLINR=222955; Pubmed=10761919; DOI=10.1038/35006655;
MEDLINR=20222555; Pubmed=10761919; DOI=10.1038/35006655;
Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M., Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T., Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S., Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A., Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehead S., Spratt B.G., Barrell B.G.;
"Complete DNA sequence of a serogroup A strain of Neisseria
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STRAIN=NG3/88;
Moe G.R., Tan S., Granoff D.M.;
Moe G.R., Tan S., Granoff D.M.;
Moe G.R., Tan S., Granoff D.M.;
Moe G.R., Tan Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";
Infect. Immun. 0:0-0(1399).
Infect. Immun. 0:0-0(1399).
HSSP; QSRP17; AF176681; AAD53284-1; -.
HSSP; QSRP17; LA4T.
GO; GO:0015288; F:porin activity; IEA.
InterPro; IPR003394; Porin activity.
PF02462; Opacity: 1.
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05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
04. Uter membrane protein.
Name=nspA; OrderedLocusNames=NMA0862;
Noisseria meninglitidis (serogroup A).
Neisseria Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
NCIS_TAXID=65699;
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98.3%; Pred. No. 2.6e-68;
ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                174 AA; 18355 MW; E8A4A1ADA4F6F009 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 404:502-506(2000).

EMBL, AL162754; CAB84143.1; --
GO; GO:0016020; C:membrane; IEA.
GO; GO:0015288; F:porin activity; IEA.
Interbro; IPR003394; Porin_opacity.
Pfam; PF02462; Opacity; I.
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01-MAY-2000 (TrEMBLrel. 13, Created)
MAY-2000 (TrEMBLrel. 13, Last sequ
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 171; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           meningitidis 22491."
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Name=nspA;
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175 AA;
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SIGNAL
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                                                                                                                                                 1 MKKALATLIALAIPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR 60
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                                                                                                                           1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                      Gaps
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Wilferences in Surface Expression of Neisserial Surface Protein A among Neisseria meningitidis Group B strains.";

Infect. Immun. 0:0-0(1999).

EMBL; AF175676; AAD53279.1; -...

EMSP; QSPR77; 194T.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0015288; F:porin activity; IEA.

DIGGEROUS IPR003394; Porin_opacity.
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                                            Length 174;
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                                                                                   3; Indels
  174 AA; 18355 MW; ECF6F38B9286800E CRC64;
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P95343;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Outer membrane protein precursor (Surface protein A).
Neisseria gonorrhoeae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                         Score 852; DB 2;
Pred. No. 3.9e-68;
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                                                                               1; Mismatches
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                                         98.2%;
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01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2003 (TrEMBLrel. 24,
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NCBI TaxID=487;
                                                                                   Matches 170; Conservative
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                                     Query Match
Best Local Similarity
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SEQUENCE
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SEQUENCE
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AC P953
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61 FAVDYTRYKNYKAPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDLGGSDSF 120
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MEDLINE-99386904; PubMed=10456958;
Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
Cadieux N., Plante M., Rioux C.R., Hamel J., Brodeur B.R., Martin D.;
Bactericidal and cross-protective activities of a monoclonal antibody
directed against Nerseria meningitidis NspA outer membrane protein.";
Infect. Immun. 67:4955-4959(1999).
EMBL; US2067; AAB41579.1;
HSSP; O9RPI7; IP4T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MKKALAALIALALPAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                                                                                                                                                                   Martin D.;
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Neisseria meningitidis.

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   Mingchun J.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18572 MW; DIEA8F2FF5CC2FEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL 1 19 Potential.
SEQUENCE 174 AA; 18337 MW; 1B558EC8A040841A CRC64;
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 825; DB 2;
Pred. No. 1e-65;
2; Mismatches
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GO; GO:0015289; F:porin activity; IEA.
InterPro; IPR003194; Porin_opacity.
Pfam; PF02462; Opacity; I.
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GO; GO:0018289; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
Pfam; PF02462; Opacity; I.
                                                                                                                                       STRAIN=B2;
MEDLINE=99270944; PubMed=10338491;
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                                                                                                                                                                                                                                                                              nfect. Immun. 67:2855-2861(1999)
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Matches 164; Conservative
                           Neisseriaceae; Neisseria
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                                                                                                               SEQUENCE FROM N.A.
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                                                      NCBI_TaxID=485;
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STRAIN=MBEL55E;
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Q51124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       115 -GGSDSFSQT---SIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSVGV 170
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                                                                                                                           1 MKKALAALIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 FAVDYTRYKNYKQVPSTDFKLYSIGASAIYDFDTQSPVKPYLGARLSLNRASVDFNGSDS
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                                                                                                   1 MKKALATLIALALPAAALAEGASGFYVQADAAHAKASSSLGSAKGFSPRISAGYRINDLR
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                                                           Gaps
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                                                                                                                                                                                                                                                                                    121 FSQTSTGLGVLAGVSYAVTPNVDLDAGYRYNYIGKVNTVKNVRSGELSAGVRVKF 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K., Kim C.H., Jeong H., Hur C.-G., Kim J.G.; "The genome sequence of the capnophilic rumen bacterium Mannheimia succiniciproducens.";
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Pasteurellaceae; Mannheimia.
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                   DB 2; Length 175;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 177 Aa; 18969 MW; BGACF0AA75915B57 CRC64;
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Last sequence update)
Last annotation update)
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    Score 824.5; DB 2;
Pred. No. 1.1e-65;
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Similarity 40.2%; Pred. No. 3.8e-19;
74; Conservative 25; Mismatches 68
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                                                           0; Mismatches
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EMBL; AE016827; AAU38304.1; -.
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25-OCT-2004 (TrEMBLrel. 28, C
25-OCT-2004 (TrEMBLrel. 28, L
25-OCT-2004 (TrEMBLrel. 28, L
Hypothetical protein.
ORFNames=MS1161;
                   95.0%;
95.4%;
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nes 74; Conservative
                                                           Matches 167; Conservative
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ORFNames=MS1697;
                                          Similarity
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                   Query Match
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Q65TE2
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Recombinational reassortment among opa genes from ET-37 complex Neisseria meningitidis isolates of diverse geographical origins.";
Microbiology 144:157-166(1998).
RMIS, 197555, AAC46101.1;
RMIS, 197737;
S77737;
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Kim C.H., Jeong H., Hur C.-G., Kim J.G.;
Kim c.H., Jeong H., Hur c.-G., Kim J.G.;
Fire genome sequence of the capnophilic rumen bacterium Mannheimia
succiniciproducens.";
Nat. Biotechnol. 0.0-0(2004).
BMBL; ABOLG827; AAU37768.1;
Hypothetical protein.
SEQUENCE 226 AA; 25460 MW; 106C558F9B4C1504 CRC64;
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Mannheimia succiniciproducens MBEL55E.
Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Mannheimia.
NCBI_TaxID=221988;
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Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
Neisseriaceae; Neisseria.
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35.1%; Pred. No. 8.6e-15;
tive 26; Mismatches 67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKKALATLIALALPAAALAEGAS-GPYVQADAAHAKASSSLGSAKG-
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01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
03coily outermembrane protein (Fragment).
Name-opa;
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Best Local Similarity
Matches 69; Conserv
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                                                                                                                                             74 PRVSVGYDFGGWRIAADYASYRKWKESNSSTKKVTEDIADNYKETKTEHQGNGSFHAASS 133
                                                                                                                                                                                                 -----ASVDLGG----- 116
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134 LGLSAIYDFKLNDKFKPYIGARVAYGHVKHQVHSVETKTTTVTSKPTATSPQGGPIIQTD 193
                                                                                                                                                                                                                                                                                            ----SDSFSQTSIGLGVLTGVSYAVTPNVDLDAGYRYNYIGKVNTVKNYRSGELSVGV 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 DLRFAVDYTRYKNYKAPS-----TDFKLYSIGASAIYDFDTQSPVKPYLGARLSLN 108
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  ---AKGFS 47
                                               14 LFSSAAQAASEDSGHGPYYVQADLAYAAERITHDYPKATGANNTSTVSDYFRNIRAHSIH 73
                                                                                               PRISAGYRINDLRFAVDYTRYK------LYS
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Pasteurellaceae; Pasteurella.
NCBI_TaxID=747;
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-----KASSSLGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 AA; 20512 MW; 1B17F0A4ACFC0157 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                               83 IGASAIYDFDTQSPVKPYLGARLSLNR-----
  LIALALPAALAEGASGFYVQADAAHA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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SEQUENCE 186 AA;
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                                                                                                                                                                                                                                                                                                                                              STRAIN=Z3524;
MEDLINE=98010345; PubMed=9350862;
Morelli G., Malorny B., Muller K., Seiler A., Wang J.F., del Valle J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Clonal descent and microevolution of Neisseria meningitidis during 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 AALAEGA-SGFYVQADAAH-----AKASSSLGS-----AKGFSPRISAGY
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                                            01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUL-1997 (TrEMBLrel. 24, Last sequence update)
Opacity protein (Fragment).
Name-opa;
Neisseria meningitidis.
Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 28.1%; Score 244; DB 2; Length 23 Best Local Similarity 28.9%; Pred. No. 1.1e-13; Matches 67; Conservative 32; Mismatches 59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         234 AA; 26134 MW; 005AD356E93BCC50 CRC64;
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234 AA
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GO, GO:0016020; C:membrane; IEA.
GO; GO:0015289; F:porin activity; IEA.
InterPro; IPR003394; Porin_opacity.
Pfam; PF02462; Opacity; 1.
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PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           years of epidemic spread.";
Mol. Microbiol. 25:1047-1064(1997)
EMBL; AF001195; AAC32716.1; -.
PRELIMINARY;
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